

PA (MITO-) MITOKOR.
 PI Anderson CM, Davis RE, Clevenger W, Wiley SE, Miller SW, Szabo TR;
 PI Ghosh SS;
 XX
 XX WPI: 2000-365619/31.
 DR N-PSDB: AAD00519.
 XX
 PT Recombinant construct encoding adenine nucleotide translocator
 PT polypeptide, useful e.g. in screening for potential therapeutic agents
 PT against mitochondrial disease -
 XX
 PS Claim 44: Page 172; 175pp; English.
 XX
 CC The patent discloses a method to produce adenine nucleotide translocator
 CC (ANT) proteins or ANT fusion proteins using recombinant expression
 CC constructs. ANT is a nuclear encoded protein and a major component of
 CC inner mitochondrial membrane. It mediates transport of adenosine
 CC d/ctri-phosphates across the mitochondrial inner membrane and also serves
 CC as an important molecular component of the mitochondrial permeability
 CC transition pore, a modulator of apoptosis. ANT is used to identify agents
 CC or ligands that bind to, or interact with it. The ANT ligands are used to
 CC detect or isolate ANT in a biological sample, and therapeutically for
 CC regulating mitochondrial pore activity, for treating diseases associated
 CC with altered mitochondrial function, including Alzheimer's, Parkinson's
 CC and Huntington's diseases, cancer, psoriasis, diabetes, dystonia,
 CC Leber's hereditary optic neuropathy, schizophrenia, mitochondrial
 CC encephalopathy, lactic acidosis and stroke (MELAS), hyperproliferative
 CC disorders, mitochondrial diabetes and deafness (MID), and myoclonic
 CC epilepsy red ragged fibre syndrome. The present sequence is an
 CC adenine nucleotide translocator ANT1 from human brain.
 XX
 SQ Sequence 297 AA;
 Query Match 100.0%; Score 1553; DB 21; Length 297;
 Best Local Similarity 100.0%; Pred. No. 3.4e-173;
 Matches 297; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MGDHANSFLKDFLAGAANAASVTAAPIERVKLLQOVHASKQISAERQKIIDCVVR 60
 DB 1 MGDHANSFLKDFLAGAANAASVTAAPIERVKLLQOVHASKQISAERQKIIDCVVR 60
 QY 61 IPKEOGFLSFWKGNLANVIRYPTQALNFAFKDKYKQLEFGVDRHKKQFWRYFAGNLASG 120
 DB 61 IPKEOGFLSFWKGNLANVIRYPTQALNFAFKDKYKQLEFGVDRHKKQFWRYFAGNLASG 120
 QY 121 GAAGATSLCFVYPLDFAFRTRLADVGRRAQREFHGLDCTIKFKSDGLNGLYOGFNVSV 180
 DB 121 GAAGATSLCFVYPLDFAFRTRLADVGRRAQREFHGLDCTIKFKSDGLNGLYOGFNVSV 180
 QY 181 OGIIIRAAVFGYDTRAKGMLPDKNVHIFVSMIAQSTYAVAGLLSYFDTYRRRMMQ 240
 DB 181 OGIIIRAAVFGYDTRAKGMLPDKNVHIFVSMIAQSTYAVAGLLSYFDTYRRRMMQ 240
 QY 241 SGRKGADIMYTGVDCKRKIAKDEGAKAFKGMASNVLRMGAGFVLYLDEIKKYV 297
 DB 241 SGRKGADIMYTGVDCKRKIAKDEGAKAFKGMASNVLRMGAGFVLYLDEIKKYV 297
 RESULT 2
 AAU01198
 ID AAU01198 standard; Protein; 297 AA.
 XX AAU01198;
 AC
 XX 07-SEP-2001 (first entry)
 DT
 XX Human adenine nucleotide translocator-1 (ANT-1) protein.
 DE
 XX Human; adenine nucleotide translocator-1; ANT-1; MTP; cyclophilin;
 KW mitochondrial permeability transition component; cell survival;
 KW mitochondrial core component; mitochondrial related disorder; cancer;
 KW Alzheimer's disease; diabetes mellitus; hyperproliferative disorder.

XX OS Homo sapiens.
 XX PN WO200132876-A2.
 XX PD 10-MAY-2001.
 XX PF 03-NOV-2000; 2000WO-US30535.
 XX PR 03-NOV-1999; 99US-0434354.
 XX
 PA (MITO-) MITOKOR.
 PI Murphy AN, Clevenger W, Wiley SE, Andreyev AV, Frigeri LG;
 PI Velicelcib G, Davis RE;
 XX
 DR WPI: 2001-291054/30.
 DR N-PSDB: AAS05901.
 XX
 PS Disclosure; Fig 2; 186pp; English.
 XX
 CC The present sequence represents human adenine nucleotide translocator-1
 CC (ANT-1) protein. ANT proteins are mitochondrial permeability
 CC transition (MTP) pore components responsible for mediating transport
 CC of ADP across the mitochondrial inner membrane. ANT proteins interact
 CC with other mitochondrial core components e.g. cyclophilins to
 CC regulate MTP. The present invention relates to a novel nucleic acid
 CC expression construct comprising a promoter operably linked to a
 CC polynucleotide encoding a mitochondrial pore component polypeptide
 CC (e.g. green fluorescent protein (GFP) or a FLASH sequence). The novel
 CC expression construct can alter mitochondrial membrane permeability
 CC transition and/or alter the interaction between mitochondrial core
 CC components. The methods are useful for screening for agents that alter
 CC MTP and/or cell survival. These agents are useful for the prevention or
 CC treatment of diseases associated with altered mitochondrial function or
 CC dysfunctional cell survival, such as Alzheimer's disease, diabetes
 CC mellitus, Parkinson's disease, Huntington's disease, schizophrenia,
 CC mitochondrial encephalopathy, lactic acidosis, stroke,
 CC hyperproliferative disorders e.g. cancer, and deafness.
 XX
 SQ Sequence 297 AA;
 Query Match 100.0%; Score 1553; DB 22; Length 297;
 Best Local Similarity 100.0%; Pred. No. 3.4e-173;
 Matches 297; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MGDHANSFLKDFLAGAANAASVTAAPIERVKLLQOVHASKQISAERQKIIDCVVR 60
 DB 1 MGDHANSFLKDFLAGAANAASVTAAPIERVKLLQOVHASKQISAERQKIIDCVVR 60
 QY 61 IPKEOGFLSFWKGNLANVIRYPTQALNFAFKDKYKQLEFGVDRHKKQFWRYFAGNLASG 120
 DB 61 IPKEOGFLSFWKGNLANVIRYPTQALNFAFKDKYKQLEFGVDRHKKQFWRYFAGNLASG 120
 QY 121 GAAGATSLCFVYPLDFAFRTRLADVGRRAQREFHGLDCTIKFKSDGLNGLYOGFNVSV 180
 DB 121 GAAGATSLCFVYPLDFAFRTRLADVGRRAQREFHGLDCTIKFKSDGLNGLYOGFNVSV 180
 QY 181 OGIIIRAAVFGYDTRAKGMLPDKNVHIFVSMIAQSTYAVAGLLSYFDTYRRRMMQ 240
 DB 181 OGIIIRAAVFGYDTRAKGMLPDKNVHIFVSMIAQSTYAVAGLLSYFDTYRRRMMQ 240
 QY 241 SGRKGADIMYTGVDCKRKIAKDEGAKAFKGMASNVLRMGAGFVLYLDEIKKYV 297
 DB 241 SGRKGADIMYTGVDCKRKIAKDEGAKAFKGMASNVLRMGAGFVLYLDEIKKYV 297

RESULT 3
AAU10378 standard; Protein: 297 AA.
AAU10378:
AAU10378:
14-FEB-2002 (first entry)
Human adenine nucleotide translocator 1 (ANT1).
Human: adenine nucleotide translocator; ANT;
mitochondrial matrix protein.
Homo sapiens.
MO200185944-A2.
15-NOV-2001.
11-MAY-2001; 2001WO-US15416.
11-MAY-2000; 2000US-0569327.
(MITO-) MITOKOR.
Anderson CM, Davis RE, Clevenger W, Wiley SE, Miller SM, Szabo TR;
P1 Ghosh SS, Moos WH, Pel Y, Carroll AK;
XX WPI: 2002-055598/07.
DR N-PSDB: AAS16688.
XX
XX Novel recombinant expression construct for producing adenine nucleotide
PT translocator polypeptides, comprises a regulated promoter linked to
PT nucleic acid encoding the polypeptide
XX
XX Claim 44; Fig 2; 147bp; English.
XX
XX The invention relates to a recombinant expression construct (I)
CC comprising a regulated promoter operably linked to a nucleic acid
CC encoding an adenine nucleotide translocator (ANT) polypeptide. ANT
CC proteins mediate the exchange of ATP synthesised in the mitochondrial
CC matrix for ADP in the cytosol. (I) is useful for producing recombinant
CC ANT polypeptide by transforming a prokaryotic or eukaryotic host cell and
CC culturing the host cell. (I) is also useful for targeting a polypeptide
CC of interest to a mitochondrial membrane, where ANT polypeptide is
CC expressed as a fusion protein with the polypeptide of interest.
CC Recombinant ANT polypeptide, or cells expressing the polypeptide, is
CC useful for identifying an agent that binds to an ANT polypeptide. ANT
CC ligand is useful for determining the presence of an ANT polypeptide,
CC preferably ANT1, ANT2 or ANT3 in a biological sample and for isolating
CC ANT from a biological sample, where the ANT ligand is covalently or non-
CC covalently bound to a solid phase. Detectably labeled ANT ligand is also
CC useful for identifying an agent that interacts with an ANT polypeptide.
CC The present sequence represents the amino acid sequence of human ANT1.
XX
SQ Sequence 297 AA:
Query Match 100.0%; Score 1553; DB 23; Length 297;
Best Local Similarity 100.0%; Pred. No. 3.4e-173;
Matches 297; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MGDHAWFLKDFLAGAANAASKTAVAPIERVKLLQVHASKQISAKQYKGIIDCYVR 60
DB 1 MGDHAWFLKDFLAGAANAASKTAVAPIERVKLLQVHASKQISAKQYKGIIDCYVR 60
QY 61 IPKEGFLSEWNGNLANYIRFPQALNFAFKDKYKQLFLGVDNRHKOFWRYFAQNLASG 120
DB 61 IPKEGFLSEWNGNLANYIRFPQALNFAFKDKYKQLFLGVDNRHKOFWRYFAQNLASG 120
QY 121 GAAGATSTCFYPPDFATRLAADYGRRAQREFHLSGCIIRKIFSSDGLRGLYQGFNVSY 180
DB 121 GAAGATSTCFYPPDFATRLAADYGRRAQREFHLSGCIIRKIFSSDGLRGLYQGFNVSY 180

QY 181 QGIIIRAAEYGVYDTAKGMLPDPKRVHIFVSWMTAQSVTAAGLSTYFPDVRRRMMQ 240
DB 181 QGIIIRAAEYGVYDTAKGMLPDPKRVHIFVSWMTAQSVTAAGLSTYFPDVRRRMMQ 240
QY 241 SGRKGADIMYTGTDCKRRIKADSGAKAFFFGANSNVLRGAGFVLYDEIKKYV 297
DB 241 SGRKGADIMYTGTDCKRRIKADSGAKAFFFGANSNVLRGAGFVLYDEIKKYV 297
RESULT 4
AAW61169 standard; Protein: 298 AA.
AAW61169:
AAW61169:
28-SEP-1998 (first entry)
Anti protein.
Anti: Adenine nucleotide translocator; cloning; screening;
KW DNA Tag diodeoxy terminator cycle sequencing; oxidative phosphorylation;
KW probe; OXPHOS; mitochondria; ADP; ATP; homozygous mutant; myopathy;
KW hypertrophic cardiomyopathy; fascioscapular humeral muscular dystrophy;
KW lactic acidosis; degenerative muscle disease.
OS Mus sp.
XX
XX WO9819714-A1.
XX 14-MAY-1998.
XX 31-OCT-1997; 97WO-US19882.
XX PF 01-NOV-1996; 96US-0030017.
XX PR (UYEM-) UNIV EMORY.
XX
XX Graham BC, Macgregor GR, Wallace DC;
XX WPI: 1998-286608/25.
XX N-PSDB: AAV36479.
XX
XX Mice lacking heart-muscle adenine nucleotide translocator protein -
PT useful as model for mitochondrial myopathy and hypertrophic
PT cardiomyopathy in animals and to test therapeutic compositions or
PT gene therapies
XX
XX Disclosure: Page 39-40; 61pp; English.
XX
XX The present sequence is the mouse Anti protein, the cDNA producing this
CC polypeptide is cloned by screening a mouse heart cDNA library with the
CC human Anti cDNA as a probe. The Anti cDNA sequence was determined by DNA
CC Tag diodeoxy terminator cycle sequencing. The Anti protein is encoded by
CC the Anti locus, a nuclear gene on chromosome 8. This protein is required
CC in mitochondrial oxidative phosphorylation (OXPHOS), as it imports ADP
CC which can then be converted into ATP. An Anti homozygous mutant would
CC thus be defective in OXPHOS which results in disease in oxidative
CC metabolism dependent tissues. This mouse Anti homozygous mutant can be
CC used as a model system for fascioscapular humeral muscular dystrophy,
CC hypertrophic cardiomyopathy, myopathy, lactic acidosis, etc. These model
CC systems can be used to test possible therapeutic compounds which
CC increase/mediate ATP and ADP exchange across the mitochondrial membrane
CC independent of ANT1.
XX
SQ Sequence 298 AA:
Query Match 93.9%; Score 1457.5; DB 19; Length 298;
Best Local Similarity 93.6%; Pred. No. 5.4e-162;
Matches 279; Conservative 10; Mismatches 8; Indels 1; Gaps 1;

QY 1 MGDHAWFLKDFLAGAANAASKTAVAPIERVKLLQVHASKQISAKQYKGIIDCYVR 60
DB 1 MGDHAWFLKDFLAGAANAASKTAVAPIERVKLLQVHASKQISAKQYKGIIDCYVR 60

| | | | |
|----|-----|---|-----|
| QY | 61 | IPPEQGFSLFPMGNLANLYRPEPTALNFAFDKTKOLELGVDRHOFMFFMFGNLSG | 120 |
| Db | 61 | IPPEQGFSLFPMGNLANLYRPEPTALNFAFDKTKOLELGVDRHOFMFFMFGNLSG | 120 |
| QY | 61 | IPPEQGFSLFPMGNLANLYRPEPTALNFAFDKTKOLELGVDRHOFMFFMFGNLSG | 120 |
| Db | 61 | IPPEQGFSLFPMGNLANLYRPEPTALNFAFDKTKOLELGVDRHOFMFFMFGNLSG | 120 |
| QY | 121 | GAAGATSLCFVYPLDFARTLADYGR-RAQREPHGLDCLIKIFKSDGLNGLYOGFNVS | 179 |
| Db | 121 | GAAGATSLCFVYPLDFARTLADYGR-RAQREPHGLDCLIKIFKSDGLNGLYOGFNVS | 179 |
| QY | 121 | GAAGATSLCFVYPLDFARTLADYGR-RAQREPHGLDCLIKIFKSDGLNGLYOGFNVS | 179 |
| Db | 121 | GAAGATSLCFVYPLDFARTLADYGR-RAQREPHGLDCLIKIFKSDGLNGLYOGFNVS | 179 |
| QY | 180 | VQGIILYRAAYGCVYDTAKGMLPDPKKNVHIIPSWHIAOSVYAVAGLLSYPPDIYRRMM | 239 |
| Db | 180 | VQGIILYRAAYGCVYDTAKGMLPDPKKNVHIIPSWHIAOSVYAVAGLLSYPPDIYRRMM | 239 |
| QY | 181 | VQGIILYRAAYGCVYDTAKGMLPDPKKNVHIIPSWHIAOSVYAVAGLLSYPPDIYRRMM | 240 |
| Db | 181 | VQGIILYRAAYGCVYDTAKGMLPDPKKNVHIIPSWHIAOSVYAVAGLLSYPPDIYRRMM | 240 |
| QY | 240 | QSGRKADIMYIGTLDCKMRKIADKGAKAFKFGANSVLRMGGAFLVLYLDELTKKYV | 297 |
| Db | 240 | QSGRKADIMYIGTLDCKMRKIADKGAKAFKFGANSVLRMGGAFLVLYLDELTKKYV | 297 |
| QY | 241 | QSGRKADIMYIGTLDCKMRKIADKGAKAFKFGANSVLRMGGAFLVLYLDELTKKYV | 298 |
| Db | 241 | QSGRKADIMYIGTLDCKMRKIADKGAKAFKFGANSVLRMGGAFLVLYLDELTKKYV | 298 |

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RESULT 5
AB053219
ID AB053219 standard; Protein; 293 AA.
XX
AC AB053219;
XX
DT 14-APR-2003 (first entry)
XX
DE Human metabolism-associated DKFZphtes3_35n12 homologue #1.
XX
KW Human; gene therapy; vaccine; disease treatment; detection.
XX
OS Homo sapiens.
XX
MO200112659-A2.
XX
PN
XX
22-FEB-2001.
XX
PE 18-AUG-2000; 2000MO-IB01496.
XX
PR 18-AUG-1999; 990S-0149499.
XX
PR 28-SEP-1999; 990S-0156503.
XX
PA (GEHD-) GERMAN HUMAN GENOME PROJECT.
XX
PI
XX
Wiemann S;
XX
WPI; 2001-327840/34.
XX
DR
XX
PT Nucleic acids having the sequences of clones isolated from libraries of
XX
PT different human tissues, useful in recombinant DNA methodologies -
XX
PS
XX
Example III; Page 850; 1095bp; English.
XX
PS
XX
This invention describes novel polynucleotides and polypeptides isolated
XX
CC from human cDNA libraries which can be used for gene therapy or in
XX
CC vaccines. The polynucleotides of the invention and antibodies encoded by
XX
CC them may be used in the prevention, diagnosis and treatment of diseases
XX
CC associated with inappropriate polypeptide expression. The products of the
XX
CC activity may also be used to identify modulators of expression and
XX
CC activity and to down regulate expression and activity. The antibodies of
XX
CC the invention may also be used as diagnostic agents for detecting the
XX
CC presence of polypeptides in samples. This sequence represents a homologue
XX
CC of a polypeptide described in the disclosure of the invention.
XX
SQ
Sequence 293 AA:
XX
Query Match 92.9%; Score 1442.5; DB 22; Length 293;
Best Local Similarity 94.2%; Pred. No. 3e-160;
Matches 276; Conservative 10; Mismatches 6; Indels 1; gaps 1
OY 5 AMSFLKDFLAGVAANAASKTAVAPLERVKLLIQVHASKDISAEKQKGIIDCVARIPE 64
b 1 AASEFLKDFLAGGIAAASVAVAPLERVKLLIQVHASKDISAEKQKGIIDCVARIPE 60

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QY 125 ATSLCFVYUPLDFAFRTYRLADVGR -RAQREPHGLADCIITKPSDGLGELYOGFVNYSVOGI 183

Db 61 QGSLSPWRNRNLNANVIRYEPPTQALNFAFDKTKQIFGLSGVDNHNKFRMYTFAGNILASGGAAG 120

QY 65 QGSLSPWRNRNLNANVIRYEPPTQALNFAFDKTKQIFGLSGVDNHNKFRMYTFAGNILASGGAAG 124

QY 121 ATSLCFVYUPLDFAFRTYRLADVKGSSQREHFNGLDCLTKIRKPSGLTKGLYOGFVSVOGI 180

Db 184 IYIRAAVFCGVYDPTATGMLPDPKNVHILFVSMIAQSVYFAVALLSPEDTYRRRRMMQSGR 243

Db 181 IYIRAAVFCGVYDPTATGMLPDPKNVHILFVSMIAQSVYFAVALLSPEDTYRRRRMMQSGR 240

QY 244 KCADIMYTGTDCWRIKIAKDEGAKAFPGAMSNNVLRGKGAGFVLYLDELTKY 296

Db 241 KCADIMYTGTDCWRIKIAKDEGAKAFPGAMSNNVLRGKGAGFVLYLDELTKY 293

| | |
|----|--|
| XX | RESULT 6 |
| XX | AA018516 |
| XX | AA018516 standard; Protein; 298 AA. |
| XX | AA018516; |
| XX | 11-OCT-2002 (first entry) |
| XX | Human Insulin receptor signaling modifier SEQ ID NO: 54. |
| XX | Human; Insulin receptor signaling; Insulin receptor signaling modifier |
| XX | ISM; diabetes; metabolic syndrome; antidiabetic. |
| XX | Homo sapiens. |
| XX | WO200255664-A2. |
| XX | 18-JUL-2002. |
| XX | 11-JAN-2002; 2002WO-US01048. |
| XX | 12-JAN-2001; 2001US-261226P. |
| XX | 12-JAN-2001; 2001US-261303P. |
| XX | 12-JAN-2001; 2001US-261304P. |
| XX | 12-JAN-2001; 2001US-261335P. |
| XX | 12-JAN-2001; 2001US-261336P. |
| XX | 12-JAN-2001; 2001US-261361P. |
| XX | 12-JAN-2001; 2001US-261456P. |
| XX | 12-JAN-2001; 2001US-261457P. |
| XX | 12-JAN-2001; 2001US-261458P. |
| XX | 12-JAN-2001; 2001US-261459P. |
| XX | 12-JAN-2001; 2001US-261518P. |
| XX | 12-JAN-2001; 2001US-261531P. |
| XX | 12-JAN-2001; 2001US-261532P. |
| XX | 12-JAN-2001; 2001US-261589P. |
| XX | 12-JAN-2001; 2001US-261590P. |
| XX | 12-JAN-2001; 2001US-261594P. |
| XX | 12-JAN-2001; 2001US-261659P. |
| XX | 12-JAN-2001; 2001US-261697P. |
| XX | (EXEL-) EXELIXIS INC. |
| XX | Seldel-Dugan C, Ferguson KC, Kidd T; |
| XX | WPI; 2002-599664/64. |
| XX | N-PSDB; AAL48635. |
| XX | Identifying an Insulin receptor signaling modulator, useful as drug |
| XX | targets for treating diabetes or metabolic disorders, comprises |
| XX | contacting an assay system comprising Insulin receptor signaling |
| XX | modifiers with a test agent - |
| XX | Disclosure; Page 160-161; 232pp; English. |
| XX | The present invention relates to a method of identifying a candidate |

CC insulin receptor (INR) signaling modulating agent, involving contacting
CC an assay system comprising an insulin receptor signaling modifier (ISM)
CC polypeptide or nucleic acid with a test agent, and detecting a test
CC agent-biased activity of the assay system. The method is useful for
CC identifying candidate INR signaling modulating agents. ISM genes may be
CC used as drug targets for treatment of disorders related to INR signaling
CC such as diabetes or metabolic syndrome. ISM nucleic acids and
CC polypeptides are useful for identifying and testing agents that modulate
CC ISM function and for other applications related to the involvement of ISM
CC in INR signaling, and for identifying subjects having a predisposition to
CC such diseases associated with INR signaling. The present sequence is an
CC ISM protein described in the exemplification of the invention.

XX Sequence 298 AA;

Query Match 90.1%; Score 1398.5; DB 23; Length 298;

Best Local Similarity 88.9%; Pred. No. 4.5e-155;

Matches 264; Conservative 17; Mismatches 15; Indels 1; Gaps 1;

QY 1 MGDHAWSEFLKDFLAGAANAASKTAVAPIERVKLLQVOHASKQISAERKYGITDCYVR 60

DB 1 MTDAAVSFAKDFLAGVAAAIKSTAVAPIERVKLLQVOHASKQITADKQYGIIDCYVR 60

QY 61 IPKQGGFLSFWRGNLANVIRYPTQALNFAFKDKYKQLFLGVDNRHKKQFWRYPAGNLASG 120

DB 61 IPKQGGFLSFWRGNLANVIRYPTQALNFAFKDKYKQLFLGVDNRHKKQFWRYPAGNLASG 120

QY 121 GAAGTSLCFEYYPIDFARTRLADYGR-AGREFHGLDCTIKIKFSGLTGYGFEVNS 179

DB 121 GAAGTSLCFEYYPIDFARTRLADYGR-AGREFHGLDCTIKIKFSGLTGYGFEVNS 180

QY 180 VQGIITVRAAYGVYDFAKGLPDPKNVHIFVSMIAQSVTAAGLSTYPTVYRRMM 239

DB 181 VQGIITVRAAYGVYDFAKGLPDPKNVHIFVSMIAQSVTAAGLSTYPTVYRRMM 240

QY 240 QSGRKADIMYTGTCWRKIAKDEGAKAFKAGANSNLRGNGAFVLVLYDEIKKY 296

DB 241 QSGRKADIMYTGTCWRKIAKDEGAKAFKAGANSNLRGNGAFVLVLYDEIKKY 297

RESULT 7

AA71032

ID AA71032 standard; Protein; 298 AA.

AC AA71032;

XX 29- AUG-2000 (first entry).

DE Human adenine nucleotide translocator ANT2.

XX Human; adenine nucleotide translocator; ANT2; mitochondria; ADP; ATP;
KW adenosine triphosphate; adenosine tri-phosphate; apoptosis; MPT; cancer;
KW mitochondrial permeability transition; neuroprotective; neurotrophic;
KW antiParkinsonian; cytoskeletal; antidiabetic; anticonvulsant; neuroleptic;
KW antipsychotic; cerebroprotective; therapeutic; psoriasis;
KW Alzheimer's disease; Parkinson's disease; Huntington's disease; dystonia;
KW diabetes; Leber's hereditary optic neuropathy; schizophrenia; MELAS;
KW mitochondrial encephalopathy; lactic acidosis; stroke; MTDD;
KW mitochondrial diabetes and deafness; hyperproliferative disorder;
KW myoclonic epilepsy red ragged fibre syndrome.

XX Homo sapiens.

OS WO200026370-A2.

PN 11-MAY-2000.

PD 03-NOV-1999; 99WO-US25883.

PF 03-NOV-1999; 98US-0185904.

PR 08-SEP-1999; 99US-0393441.

XX (MITO-) MITOKOR.

XX Anderson CM, Davis RE, Clevenger W, Wiley SE, Miller SW, Szabo TR;
PI Ghosh SS;

DR WPT: 2000-365619/31.

DR N-PDB: AAD00520.

XX Recombinant construct encoding adenine nucleotide translocator
PR polypeptide, useful e.g. in screening for potential therapeutic agents
PT against mitochondrial disease

XX Claim 45; Page 172-173; 175pp; English.

XX The patent discloses a method to produce adenine nucleotide translocator
CC (ANT) proteins or ANT fusion proteins using recombinant expression
CC constructs. ANT is a nuclear encoded protein and a major component of
CC inner mitochondrial membrane. It mediates transport of adenosine
CC di/tri-phosphates across the mitochondrial inner membrane and also serves
CC as an important molecular component of the mitochondrial permeability
CC transition pore, a modulator of apoptosis. ANT is used to identify agents
CC or ligands that bind to, or interact with it. The ANT ligands are used to
CC detect or isolate ANT in a biological sample, and therapeutically for
CC regulating mitochondrial pore activity, for treating diseases associated
CC with altered mitochondrial function, including Alzheimer's, Parkinson's
CC and Huntington's diseases, cancer, psoriasis, diabetes, dystonia,
CC Leber's hereditary optic neuropathy, schizophrenia, mitochondrial
CC encephalopathy, lactic acidosis and stroke (MELAS), hyperproliferative
CC disorders, mitochondrial diabetes and deafness (MTDD), and myoclonic
CC epilepsy red ragged fibre syndrome. The present sequence is an
CC adenine nucleotide translocator ANT2 from human brain.

SQ Sequence 298 AA;

Query Match 89.6%; Score 1391.5; DB 21; Length 298;

Best Local Similarity 88.6%; Pred. No. 3e-154;

Matches 263; Conservative 17; Mismatches 16; Indels 1; Gaps 1;

QY 1 MGDHAWSEFLKDFLAGAANAASKTAVAPIERVKLLQVOHASKQISAERKYGITDCYVR 60

DB 1 MTDAAVSFAKDFLAGVAAAIKSTAVAPIERVKLLQVOHASKQITADKQYGIIDCYVR 60

QY 61 IPKQGGFLSFWRGNLANVIRYPTQALNFAFKDKYKQLFLGVDNRHKKQFWRYPAGNLASG 120

DB 61 IPKQGGFLSFWRGNLANVIRYPTQALNFAFKDKYKQLFLGVDNRHKKQFWRYPAGNLASG 120

QY 121 GAAGTSLCFEYYPIDFARTRLADYGR-AGREFHGLDCTIKIKFSGLTGYGFEVNS 179

DB 121 GAAGTSLCFEYYPIDFARTRLADYGR-AGREFHGLDCTIKIKFSGLTGYGFEVNS 180

QY 180 VQGIITVRAAYGVYDFAKGLPDPKNVHIFVSMIAQSVTAAGLSTYPTVYRRMM 239

DB 181 VQGIITVRAAYGVYDFAKGLPDPKNVHIFVSMIAQSVTAAGLSTYPTVYRRMM 240

QY 240 QSGRKADIMYTGTCWRKIAKDEGAKAFKAGANSNLRGNGAFVLVLYDEIKKY 296

DB 241 QSGRKADIMYTGTCWRKIAKDEGAKAFKAGANSNLRGNGAFVLVLYDEIKKY 297

RESULT 8

AAU01199

ID AAU01199 standard; Protein; 298 AA.

AC AAU01199;

XX 07-SEP-2001 (first entry)

DE Human adenine nucleotide translocator-2 (ANT-2) protein.

XX Human; adenine nucleotide translocator-2; ANT-2; MPT; cyclophilin;
KW mitochondrial permeability transition pore component; cell survival;
KW mitochondrial core component; mitochondrial related disorder; cancer;
KW Alzheimer's disease; diabetes mellitus; hyperproliferative disorder.

OS Homo sapiens.
PN WO200132876-A2.
XX 10-MAY-2001.
PD
XX 03-NOV-2000; 2000WO-US030535.
PE
XX 03-NOV-1999; 99US-0434354.
PR
XX (MITO-) MITOKOR.
PA
PI Murphy AN, Clevenger W, Wiley SE, Andreyev AY, Frigeri LG;
PI Velicelceti G, Davis RE;
DR WPI; 2001-291054/30.
DR N-PSDB; AAS05902.
XX
XX New nucleic acid expression constructs, useful for screening for agents
PT that alter mitochondrial permeability transition (MPT), comprises
PT polynucleotide encoding MPT polypeptide or cyclophilin polypeptide
PT fused to energy transfer molecule -
PS
XX Disclosure; Fig 2; 186pp; English.
XX
XX The present sequence represents human adenine nucleotide translocator-2
CC (ANT-2) protein. ANT proteins are mitochondrial permeability
CC transition (MPT) pore components responsible for mediating transport
CC of ADP across the mitochondrial inner membrane. ANT proteins interact
CC with other mitochondrial core components e.g. cyclophilins to
CC regulate MPT. The present invention relates to a novel nucleic acid
CC expression construct comprising a promoter operably linked to a
CC polynucleotide encoding a mitochondrial pore component polypeptide
CC (e.g. ANT) fused to an energy transfer molecule (ETM) protein
CC (e.g. green fluorescent protein (GFP) or a FLASH sequence). The novel
CC expression construct can alter mitochondrial membrane permeability
CC transition and/or alter the interaction between mitochondrial core
CC components. The methods are useful for screening for agents that alter
CC MPT and/or cell survival. These agents are useful for the prevention or
CC treatment of diseases associated with altered mitochondrial function or
CC dysfunctional cell survival, such as Alzheimer's disease, diabetes
CC mellitus, Parkinson's disease, Huntington's disease, schizophrenia,
CC mitochondrial encephalopathy, lactic acidosis, stroke,
CC hyperproliferative disorders e.g. cancer, and deafness.
XX
SQ Sequence 298 AA;
Query Match 89.6%; Score 1391.5; DB 22; Length 298;
Best Local Similarity 88.6%; Pred. No. 3e-154;
Matches 263; Conservative 17; Mismatches 16; Indels 1; Gaps 1;
QY 1 MGDHANSFLKDLGAGVAAVSTKTAAPLIERVKLLQOVHASKQISAEKQYKGIIDCVVR 60
1 MTDAAISFPAKDFLAGVAAVSTKTAAPLIERVKLLQOVHASKQITADKQYKGIIDCVVR 60
DB
QY 61 IPKEQGLSFWRGNLNVIRYPTQALNFAFKQYKQFLGVDKRFKQFRYRAGNLAG 120
1 IPKEQGLSFWRGNLNVIRYPTQALNFAFKQYKQFLGVDKRFKQFRYRAGNLAG 120
DB 61 IPKEQGLSFWRGNLNVIRYPTQALNFAFKQYKQFLGVDKRFKQFRYRAGNLAG 120
QY 121 GAAGATSLCFVPLDFAFRTLRADVGR-AQREFHGLGDCIIRKFSKDGRLGYOGFNVS 179
121 GAAGATSLCFVPLDFAFRTLRADVGR-AQREFHGLGDCIIRKFSKDGRLGYOGFNVS 179
DB 121 GAAGATSLCFVPLDFAFRTLRADVGR-AQREFHGLGDCIIRKFSKDGRLGYOGFNVS 180
121 GAAGATSLCFVPLDFAFRTLRADVGR-AQREFHGLGDCIIRKFSKDGRLGYOGFNVS 180
QY 180 VGGIITIRAAVFGVDTAKGMLPDPKNVHIFVSMIAQSVTAVAGLLSTPFTVRRRMM 239
180 VGGIITIRAAVFGVDTAKGMLPDPKNVHIFVSMIAQSVTAVAGLLSTPFTVRRRMM 239
DB 181 VGGIITIRAAVFGVDTAKGMLPDPKNVHIFVSMIAQSVTAVAGLLSTPFTVRRRMM 240
181 VGGIITIRAAVFGVDTAKGMLPDPKNVHIFVSMIAQSVTAVAGLLSTPFTVRRRMM 240
QY 240 QSRKRGADIVTGTVCWKRIADDEGAKAFKFGKAGSNVLRGSGAVLVLYDEIKKY 296
240 QSRKRGADIVTGTVCWKRIADDEGAKAFKFGKAGSNVLRGSGAVLVLYDEIKKY 296
DB 241 QSRKRGADIVTGTVCWKRIADDEGAKAFKFGKAGSNVLRGSGAVLVLYDEIKKY 297
241 QSRKRGADIVTGTVCWKRIADDEGAKAFKFGKAGSNVLRGSGAVLVLYDEIKKY 297
RESULT 9

AAU10379
ID AAU10379 standard; Protein; 298 AA.
XX
XX AAU10379;
AC
XX
XX 14-FEB-2002 (first entry)
DT
XX
XX Human adenine nucleotide translocator 2 (ANT2).
DE
XX
XX Human; adenine nucleotide translocator; ANT; ss;
KM
XX
XX mitochondrial matrix protein.
XX
OS Homo sapiens.
XX
XX WO200185944-A2.
PN
XX
XX 15-NOV-2001.
PD
XX
XX 11-MAY-2001; 2001WO-US15416.
PE
XX
XX 11-MAY-2000; 2000US-0569327.
PR
XX
XX (MITO-) MITOKOR.
PA
XX
XX Anderson CM, Davis RE, Clevenger W, Wiley SE, Miller SM, Szabo TR;
PI Ghosh SS, Moos WH, Pei Y, Carroll AK;
PI WPI; 2002-055598/07.
DR N-PSDB; AAS16689.
DR
XX
XX Novel recombinant expression construct for producing adenine nucleotide
PT translocator polypeptides, comprises a regulated promoter linked to
PT nucleic acid encoding the polypeptide -
PS
XX Claim 44; Fig 2; 147pp; English.
XX
XX The invention relates to a recombinant expression construct (1)
CC comprising a regulated promoter operably linked to a nucleic acid
CC encoding an adenine nucleotide translocator (ANT) polypeptide. ANT
CC proteins mediate the exchange of ADP synthesised in the mitochondrial
CC matrix for ADP in the cytosol. (1) is useful for producing recombinant
CC ANT polypeptide by transforming a prokaryotic or eukaryotic host cell and
CC culturing the host cell. (1) is also useful for targeting a polypeptide
CC of interest to a mitochondrial membrane, where ANT polypeptide is
CC expressed as a fusion protein with the polypeptide of interest.
CC Recombinant ANT polypeptide, or cells expressing the polypeptide, is
CC useful for identifying an agent that binds to an ANT polypeptide. ANT
CC ligand is useful for determining the presence of an ANT polypeptide,
CC preferably ANT1, ANT2 or ANT3 in a biological sample and for isolating
CC ANT from a biological sample, where the ANT ligand is covalently or non-
CC covalently bound to a solid phase. Detectably labeled ANT ligand is also
CC useful for identifying an agent that interacts with an ANT polypeptide.
CC The present sequence represents the amino acid sequence of human ANT2.
XX
SQ Sequence 298 AA;
Query Match 89.6%; Score 1391.5; DB 23; Length 298;
Best Local Similarity 88.6%; Pred. No. 3e-154;
Matches 263; Conservative 17; Mismatches 16; Indels 1; Gaps 1;
QY 1 MGDHANSFLKDLGAGVAAVSTKTAAPLIERVKLLQOVHASKQISAEKQYKGIIDCVVR 60
1 MTDAAISFPAKDFLAGVAAVSTKTAAPLIERVKLLQOVHASKQITADKQYKGIIDCVVR 60
DB
QY 61 IPKEQGLSFWRGNLNVIRYPTQALNFAFKQYKQFLGVDKRFKQFRYRAGNLAG 120
1 IPKEQGLSFWRGNLNVIRYPTQALNFAFKQYKQFLGVDKRFKQFRYRAGNLAG 120
DB 61 IPKEQGLSFWRGNLNVIRYPTQALNFAFKQYKQFLGVDKRFKQFRYRAGNLAG 120
QY 121 GAAGATSLCFVPLDFAFRTLRADVGR-AQREFHGLGDCIIRKFSKDGRLGYOGFNVS 179
121 GAAGATSLCFVPLDFAFRTLRADVGR-AQREFHGLGDCIIRKFSKDGRLGYOGFNVS 179
DB 121 GAAGATSLCFVPLDFAFRTLRADVGR-AQREFHGLGDCIIRKFSKDGRLGYOGFNVS 180
121 GAAGATSLCFVPLDFAFRTLRADVGR-AQREFHGLGDCIIRKFSKDGRLGYOGFNVS 180
QY 180 VGGIITIRAAVFGVDTAKGMLPDPKNVHIFVSMIAQSVTAVAGLLSTPFTVRRRMM 239
180 VGGIITIRAAVFGVDTAKGMLPDPKNVHIFVSMIAQSVTAVAGLLSTPFTVRRRMM 239

|||||
DB 181 VGGIITRAAYFGVYDFAKGM.LPDPKNTIYISWMIAGTVAVAGLTSYPEDTVRRMM 240
OY 240 OSGRGADIMYTGTVDCMRKTADEGAKAFKAGMSNVLKMGAFVLYLDEIKKY 296
DB 241 OSGRGADIMYTGTVDCMRKTADEGAKAFKAGMSNVLKMGAFVLYLDEIKKY 297
RESULT 10
AAY71033
ID AAY71033 standard; Protein: 298 AA.
XX AAY71033;
AC
XX
XX
XX 29-AUG-2000 (first entry)
DE Human adenine nucleotide translocator ANT3.
XX
XX Human; adenine nucleotide translocator; ANT3; mitochondria; ADP; ATP;
KW adenosine di-phosphate; adenosine tri-phosphate; apoptosis; MPT; cancer;
KW mitochondrial permeability transition; neuroprotective; neurotropic;
KW antiParkinsonian; cytosolic; antidiabetic; anticonvulsant; neuroleptic;
KW antiparkinsonic; cerebroprotective; therapeutic; screening; psoriasis;
KW Alzheimer's disease; Parkinson's disease; Huntington's disease; dystonia;
KW diabetes; Leber's hereditary optic neuropathy; schizophrenia; MELAS;
KW mitochondrial encephalopathy; lactic acidosis; stroke; MIDD;
KW mitochondrial diabetes and deafness; hyperproliferative disorder;
KW myoclonic epilepsy red ragged fibre syndrome.
XX
XX Homo sapiens.
OS
XX WO200026370-A2.
XX
XX 11-MAY-2000.
XX
XX 03-NOV-1999; 99WO-US25883.
XX
XX 03-NOV-1999; 98US-0185904.
XX 08-SEP-1999; 99US-0393441.
XX
XX (MITO-) MITOKOR.
XX
XX Anderson CM, Davis RE, Clevenger W, Wiley SE, Miller SW, Szabo TR;
PI Ghosh SS;
XX
XX MPI: 2000-365619/31.
XX
XX N-PSDB: AAD00521.
XX
XX Recombinant construct encoding adenine nucleotide translocator
PT polypeptide, useful e.g. in screening for potential therapeutic agents
PT against mitochondrial disease -
XX
XX
XX Claim 46; Page 173-174; 175pp; English.
XX
XX The patent discloses a method to produce adenine nucleotide translocator
CC (ANT) proteins or ANT fusion proteins using recombinant expression
CC constructs. ANT is a nuclear encoded protein and a major component of
CC inner mitochondrial membrane. It mediates transport of adenosine
CC di/tri-phosphates across the mitochondrial inner membrane and also serves
CC as an important molecular component of the mitochondrial permeability
CC transition pore, a modulator of apoptosis. ANT is used to identify agents
CC or ligands that bind to, or interact with it. The ANT ligands are used to
CC detect or isolate ANT in a biological sample, and therapeutically for
CC regulating mitochondrial pore activity, for treating diseases associated
CC with altered mitochondrial function, including Alzheimer's, Parkinson's
CC and Huntington's diseases, cancer, psoriasis, diabetes, dystonia,
CC Leber's hereditary optic neuropathy, schizophrenia, mitochondrial
CC encephalopathy, lactic acidosis and stroke (MELAS), hyperproliferative
CC disorders, mitochondrial diabetes and deafness (MIDD), and myoclonic
CC epilepsy red ragged fibre syndrome. The present sequence is an
CC adenine nucleotide translocator ANT3 from human brain.
XX
XX Sequence 298 AA;

Query Match 89.2%; Score 1385.5; DB 21; Length 298;
Best Local Similarity 87.2%; Pred No. 1.5e-153;
Matches 260; Conservative 21; Mismatches 16; Indels 1; Gaps 1;
OY 1 MGDHMSFLKDFLAGAANAASKTAVAPIERVKLLQVOHASKQISAKQYKGIIDCYVR 60
DB 1 MTEQATSPAKDFLAGIAAASKTAVAPIERVKLLQVOHASKQIAADKQYKGIIDCYVR 60
OY 61 IPKEGGLTFWFGNLANVIRIFPTQALNFAEDKTKQFLGCVDRHKKQFWYFAGNLAG 120
DB 61 IPKEGGLTFWFGNLANVIRIFPTQALNFAEDKTKQFLGCVDRHKKQFWYFAGNLAG 120
OY 121 GAAGATSCFYVPLDFAPTRIAADYGR-ADKEEFGIDCIIKPSGRLGCGFVNS 179
DB 121 GAAGATSCFYVPLDFAPTRIAADYGR-ADKEEFGIDCIIKPSGRLGCGFVNS 180
OY 180 VGGIITRAAYFGVYDFAKGM.LPDPKNTIYISWMIAGTVAVAGLTSYPEDTVRRMM 239
DB 181 VGGIITRAAYFGVYDFAKGM.LPDPKNTIYISWMIAGTVAVAGVSPEDTVRRMM 240
OY 240 OSGRGADIMYTGTVDCMRKTADEGAKAFKAGMSNVLKMGAFVLYLDEIKKY 297
DB 241 OSGRGADIMYTGTVDCMRKTADEGAKAFKAGMSNVLKMGAFVLYLDEIKKY 298
RESULT 11
AAM39641
ID AAM39641 standard; Protein: 298 AA.
XX
XX AAM39641;
AC
XX
XX 22-OCT-2001 (first entry)
DE
XX
XX Human polypeptide SEQ ID NO 2786.
DE
XX
XX Human; neurotropic; immunosuppressant; cytostatic; gene therapy; cancer;
KW peripheral nervous system; neuropathy; central nervous system; CNS;
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotoxic;
KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
KW leukaemia.
XX
XX Homo sapiens.
OS
XX WO200153312-A1.
XX
XX 26-JUL-2001.
XX
XX 26-DEC-2000; 2000WO-US34263.
XX
XX 21-JAN-2000; 2000US-0488725.
XX 25-APR-2000; 2000US-0552317.
XX 09-JUL-2000; 2000US-0598042.
XX 19-JUL-2000; 2000US-0620312.
XX 03-AUG-2000; 2000US-0653450.
XX 14-SEP-2000; 2000US-0662191.
XX 19-OCT-2000; 2000US-0693036.
XX 29-NOV-2000; 2000US-0727344.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
PI Zhao Q, Zhou P, Goodrich R, Drmanac RT;
XX
XX MPI: 2001-442253/47.
XX
XX N-PSDB: AAI58797.
XX
XX Novel nucleic acids and polypeptides, useful for treating disorders
PT such as central nervous system injuries -
XX
XX Example 4; SEQ ID NO 2786; 10078pp; English.
PS

| XX | PN | WO200185944-A2. |
|-----------------------|------------------|---|
| XX | XX | 15-NOV-2001. |
| XX | XX | 11-MAY-2001; 2001WO-US15416. |
| XX | XX | 11-MAY-2000; 2000US-0569327. |
| XX | XX | (MITO-) MITOKOR. |
| XX | XX | Anderson CM, Davis RE, Clevenger W, Wiley SE, Miller SW, Szabo TR; |
| XX | XX | Ghosh SS, Moos WH, Pel Y, Carroll AK; |
| XX | XX | WPI: 2002-055598/07. |
| XX | XX | N-PSDB: AAS16690. |
| PT | PT | Novel recombinant expression construct for producing adenine nucleotide |
| PT | PT | translocator polypeptides, comprises a regulated promoter linked to |
| PT | PT | nucleic acid encoding the polypeptide |
| XX | XX | Example 3; Fig 2; 147p; English. |
| CC | CC | The invention relates to a recombinant expression construct (I) |
| CC | CC | comprising a regulated promoter operably linked to a nucleic acid |
| CC | CC | encoding an adenine nucleotide translocator (ANT) polypeptide. ANT |
| CC | CC | proteins mediate the exchange of ATP synthesised in the mitochondrial |
| CC | CC | matrix for ADP in the cytosol. (I) is useful for producing recombinant |
| CC | CC | ANT polypeptide by transforming a prokaryotic or eukaryotic host cell and |
| CC | CC | culturing the host cell. (I) is also useful for targeting a polypeptide |
| CC | CC | of interest to a mitochondrial membrane, where ANT polypeptide is |
| CC | CC | expressed as a fusion protein with the polypeptide of interest. |
| CC | CC | Recombinant ANT polypeptide, or cells expressing the polypeptide, is |
| CC | CC | useful for identifying an agent that binds to an ANT polypeptide. ANT |
| CC | CC | ligand is useful for determining the presence of an ANT polypeptide. |
| CC | CC | preferably ANT1, ANT2 or ANT3 in a biological sample and for isolating |
| CC | CC | ANT from a biological sample, where the ANT ligand is covalently or non- |
| CC | CC | covalently bound to a solid phase. Detectably labeled ANT ligand is also |
| CC | CC | useful for identifying an agent that interacts with an ANT polypeptide. |
| CC | CC | The present sequence represents the amino acid sequence of human ANT3. |
| SO | SO | Sequence 298 AA; |
| Query Match | 89.2%; | Score 1385.5; DB 23; Length 298; |
| Best Local Similarity | 87.2%; | Pred. No. 1.5e-153; |
| Matches 260; | Conservative 21; | Mismatches 16; Indels 1; Gaps 1 |
| OY | 1 | MGDAWSTLKEFLGAVAAAVSKTPVAATIERVKLLLOVQHASKQISAERKGYGIIIDCYVR 60 |
| DB | 1 | MTEDALISPAKQFLGAGIAAASIKTAVAATIERVKLLLOVQHASKQIAADQYGVYDCIVR 60 |
| OY | 61 | IPKEGELTFWRGNLANVIRYFPTQALNFAAFDKKQKQLFLGVDNRHKKQFWRFPAGNIASG 120 |
| DB | 61 | IPKQGVSLTFWRGNLANVIRYFPTQALNFAAFDKKQKQLFLGVDNRHKKQFWRFPAGNIASG 120 |
| OY | 121 | GAAQATSLCFVYPLDFEARTRLAADVGR-AQREFHGLDCCIIRKESDGLRGLYOGFNVS 179 |
| DB | 121 | GAAQATSLCFVYPLDFEARTRLAADVGRSGTEREFGRLGDLIVKIRKSDGIRGLYOGFSVS 180 |
| OY | 180 | VQGIITVYAAAFVGYDTRAKGMLPDKKNVHIEVSMIAQSVYAVAGLSTPEPTVRRRRMM 239 |
| DB | 181 | VQGIITVYAAAFVGYDTRAKGMLPDKKNVHIEVSMIAQSVYAVAGLSTPEPTVRRRRMM 240 |
| OY | 240 | QSGRGADIMYTGVDCKRIAKDGAFAEFKGSNVLRGGAFAVLVLYDEIKKYY 297 |
| DB | 241 | QSGRGADIMYTGVDCKRIAKDGAFAEFKGSNVLRGGAFAVLVLYDEIKKVI 298 |
| RESULT 14 | | |
| ID | AA041427 | standard; Protein; 323 AA. |
| NC | AA041427; | |

```
XX XX      22-Oct-2001   (first entry)
XX DE
XX DE      Human polypeptide SEQ ID NO 6358.
XX XX
KW Human; nocotropic; immunosuppressant; cytotactic; gene therapy; cancer;
KW peripheral nervous system; neuropathy; central nervous system; CNS;
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW amyotrophic lateral sclerosis; Shy-Dreager Syndrome; chemotactic;
KW chemokinetic; thrombolytic; drug screening; arthritis; inflammation;
KW leukaemia.
XX XX
OS Homo sapiens.
XX PN       WO200153312-A1.
XX PD
XX PF       26-Jul-2001.
XX PE
XX PF       26-Dec-2000; 2000MO-US34263.
XX PR
XX PR       21-Jan-2000; 2000US-0488725.
XX PR       25-Apr-2000; 2000US-0552317.
XX PR       09-Jul-2000; 2000US-0598042.
XX PR       19-Jul-2000; 2000US-0620312.
XX PR       03-Aug-2000; 2000US-0653450.
XX PR       14-Sep-2000; 2000US-0662191.
XX PR       19-Oct-2000; 2000US-0693036.
XX PR       29-Nov-2000; 2000US-0727344.
XX PA
XX PA       (HYSEQ-) HYSEQ INC.
XX PI
XX PI       Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
PI         Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
PI         Zhao QA, Zhou P, Goodrich R, Drmanac RT;
XX XX
XX WI       WPI: 2001-442253/47.
XX DR
XX DR       N-PDB: AAI60383.
XX PT
XX PT       Novel nucleic acids and polypeptides, useful for treating disorders
PT     such as central nervous system injuries -
PS PS       Example 2; SEQ ID NO 6358; 10078bp; English.
XX XX
XX XX       The invention relates to human nucleic acids (AAI57798-AAI61369) and
CC       the encoded polypeptides (AAM38642-AMA42213) with nocrotropic.
CC       immunosuppressant and cytotoxic activity. The polynucleotides are useful
CC       in gene therapy. A composition containing a polypeptide or polynucleotide
CC       of the invention may be used to treat diseases of the peripheral nervous
CC       system, such as peripheral nervous injuries, peripheral neuropathy and
CC       localized neuropathies and central nervous system diseases, such as
CC       Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC       lateral sclerosis, and Shy-Dreager Syndrome. Other uses include the
CC       utilisation of the activities such as: Immune system suppression,
CC       Activin/inhibin activity, chemotactic/chemokine activity, haemostatic
CC       and thrombotic activity, cancer diagnosis and therapy, drug screening,
CC       assays for receptor activity, arthritis and inflammation, leukemias and
CC       C.N.S disorders.
CC CC       Note: The sequence data for this patent did not form part of the printed
CC specification.
XX XX
SQ Sequence    323 AA;
Query Match          89.2%; Score 1385.5; DB 22; Length 323;
Best Local Similarity 87.2%; Pred. No. 17e-153;
Matches 260; Conservative 21; Mismatches 16; Indels 1; Gaps 1
DB 1  MGDHAWFLDPLAGVAAAASVTAVAPIERKLLIOVOHASKOISAEQYKGIIDCVR 60
| : | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 26  MTEGATSFANDFLAGGAIAASTRTVAPIERKLLLOVHASKOIAADKKGVDCIVR 85
        1  IPKEQGSLSWRGRLANVRIRPFTOALNFAFDKTKQLFGLGVDRHKOFRRYPFGNTASG 1200
IPKKGSLSPWRGNLANVRIRPFTOALNFAFDKTKQLFGLGVDRHKOFRRYPFGNTASG 1455
```

QY 121 GAAGATSLCFVYPLDFAFRLADVGR-AQREFHGLGDCIIFKPSDGLRGLYGFNVS 179
 |||||
 DB 146 GAAGATSLCFVYPLDFAFRLADVGR-KSGEREFRLGDLVITKSDGIRGLYGFNVS 205
 QY 180 VGGIITIRAAVEGYDTAKGMLPDPKRVHIFVSMIAQSYTAVAGLSTYEDTVRRRMM 239
 |||||
 DB 206 VGGIITIRAAVEGYDTAKGMLPDPKRVHIFVSMIAQSYTAVAGLSTYEDTVRRRMM 265
 QY 240 QSGRKGADIMYTGTVDCKRKIADEGAKAFKFGKAMSNTLRGMCAPVLYLYDEIKKYV 297
 |||||
 DB 266 QSGRKGADIMYTGTVDCKRKIFDEGKAFKFGKAMSNTLRGMCAPVLYLYDEIKKYV 323

RESULT 15
 ID ABG15423 standard; Protein; 325 AA.
 AC ABG15423;
 XX 18-FEB-2002 (first entry)
 DE Novel human diagnostic protein #15414.
 XX Human; chromosome mapping; gene mapping; gene therapy; forensic;
 KW Food supplement; medical imaging; diagnostic; genetic disorder.
 XX Homo sapiens.
 OS WO200175067-A2.
 PN 11-OCT-2001.
 PD 30-MAR-2001; 2001WO-0508631.
 PF 31-MAR-2000; 2000US-0540217.
 PR 23-AUG-2000; 2000US-0649167.
 PA (HYSE-) HYSEQ INC.
 PI Drmanac RT, Liu C, Tang YT:
 XX WPI; 2001-639362/73.
 DR N-PSDB; AAS79610.
 XX

New isolated polynucleotide and encoded polypeptides, useful in
 PT diagnostics, forensics, gene mapping, identification of mutations
 PT responsible for genetic disorders or other traits and to assess
 PT biodiversity -
 XX

Claim 20: SEQ ID No 45782; 103pp: English.

The invention relates to isolated polynucleotide (I) and
 CC polypeptide (II) sequences. (I) is useful as hybridisation probes,
 CC polymerase chain reaction (PCR) primers, oligomers, and for chromosome
 CC and gene mapping, and in recombinant production of (II). The
 CC polynucleotides are also used in diagnostics as expressed sequence tags
 CC for identifying expressed genes. (I) is useful in gene therapy techniques
 CC to restore normal activity of (II) or to treat disease states involving
 CC (II). (II) is useful for generating antibodies against it, detecting or
 CC quantitating a polypeptide in tissue, as molecular weight markers and as
 CC a food supplement. (II) and its binding partners are useful in medical
 CC imaging of sites expressing (II). (I) and (II) are useful for treating
 CC disorders involving aberrant protein expression or biological activity.
 CC The polypeptide and polynucleotide sequences have applications in
 CC diagnostics, forensics, gene mapping, identification of mutations
 CC responsible for genetic disorders or other traits to assess biodiversity
 CC and to produce other types of data and products dependent on DNA and
 CC amino acid sequences. ABG00010-ABG30377 represent novel human
 CC diagnostic amino acid sequences of the invention.
 CC Note: The sequence data for this patent did not appear in the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pct_sequences.

XX SQ Sequence 325 AA;
 Query Match 83.4%; Score 1294.5; DB 22; Length 325;
 Best Local Similarity 83.4%; Pred. No. 8e-143;
 Matches 251; Conservative 19; Mismatches 26; Indels 5; Gaps 4;

QY 1 MGDHASFLLKDFLAGAFAAASVTAAVPIERVLLQVHASKQISAERKQKIIDCVVR 60
 |||||
 DB 24 MTDAAVSPAKDFLAGVAAAIKSTVAPIERVLLQVHASKQIADAKQKIIICVVR 83
 QY 61 IPKEGFLSFWRGNLANVIRYFPTQALNFAKDKYQLEFLGVDRKKQFWRFAGNLASG 120
 |||||
 DB 84 IPKEGFLSFWRGNLANVIRYFPTQALNFAKDKYQIFLGVDKRTQFWRFARNLASG 143

QY 121 GAAGATSLCFVYPLDFAFRLADVGR-AQREFHGLGDCIIFKPSDGLRGLYGFNVS 179
 |||||
 DB 144 GAAGATSLCFVYPLDFAFRLADVGR-KSGEREFRLGDLVITKSDGIRGLYGFNVS 203

QY 180 VGGIITIRAAVEGYDTAKGMLPDPKRVHIFVSMIAQSYTAVAGLSTYEDTVRRR 236
 |||||
 DB 204 VGGIITIRAAVEGYDTAKGMLPDPKRVHIFVSMIAQSYTAVAGLSTYEDTVRRR 263

QY 237 MMQSGRKGADIMYTGTVDCKRKIADEGAKAFKFGKAMSNTLRGMCAPVLYLYD-EIKK 295
 |||||
 DB 264 EXMQSGRKGADIMYTGTVDCKRKIADEGAKAFKFGKAMSNTLRGMCAPVLYLYEXKSKK 323

QY 296 Y 296
 DB 324 Y 324

Search completed: August 28, 2003, 19:38:47
 Job time : 53.2161 secs

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OM protein - protein search, using sw model

Run on: August 28, 2003, 19:36:11 : Search time 17.9597 Seconds
(without alignments)
699.696 Million cell updates/sec

Title: US-09-811-132-31

Perfect score: 1553
Sequence: 1 MGDHMSFLKDFLAGAATAA.....LNGMGARVLYLDEIKKYV 297

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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4: /cgn2_6/prodata/1/1aa/6B.COMB.pep:*
5: /cgn2_6/prodata/1/1aa/PCUTS.COMB.pep:*
6: /cgn2_6/prodata/1/1aa/Backfilest1.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|--------|-------------|--------|-------|--------------------|
| 1 | 1553 | 100.0 | 297 | 4 | US-09-434-354-47 |
| 2 | 1457.5 | 93.9 | 298 | 3 | US-08-961-871-10 |
| 3 | 1391.5 | 89.6 | 298 | 4 | US-09-434-354-48 |
| 4 | 1385.5 | 89.2 | 298 | 4 | US-09-434-354-48 |
| 5 | 304 | 19.6 | 469 | 4 | US-09-996-243-289 |
| 6 | 301 | 19.4 | 469 | 3 | US-09-188-930-339 |
| 7 | 301 | 19.4 | 469 | 4 | US-09-312-283C-339 |
| 8 | 281 | 18.7 | 447 | 4 | US-09-160-119-4 |
| 9 | 281 | 18.7 | 447 | 4 | US-09-160-119-4 |
| 10 | 267 | 17.2 | 674 | 4 | US-09-501-558-2 |
| 11 | 265.5 | 17.1 | 291 | 4 | US-09-482-273-118 |
| 12 | 238 | 15.3 | 320 | 2 | US-08-933-750C-112 |
| 13 | 238 | 15.3 | 320 | 3 | US-09-334-613-12 |
| 14 | 233.5 | 15.0 | 312 | 3 | US-09-142-565-2 |
| 15 | 227 | 14.6 | 299 | 1 | US-08-518-878B-56 |
| 16 | 227 | 14.6 | 299 | 2 | US-08-470-868A-56 |
| 17 | 227 | 14.6 | 309 | 1 | US-08-518-878B-51 |
| 18 | 227 | 14.6 | 309 | 2 | US-08-807-861A-51 |
| 19 | 227 | 14.6 | 309 | 2 | US-08-470-868A-51 |
| 20 | 227 | 14.6 | 309 | 3 | US-09-210-681-51 |
| 21 | 227 | 14.6 | 309 | 3 | US-08-946-719A-51 |
| 22 | 227 | 14.6 | 309 | 4 | US-09-547-983-51 |
| 23 | 225 | 14.5 | 311 | 2 | US-08-775-009-33 |
| 24 | 225 | 14.5 | 311 | 2 | US-08-775-009-33 |
| 25 | 222.5 | 14.3 | 308 | 2 | US-08-937-466-2 |
| 26 | 222.5 | 14.3 | 308 | 2 | US-09-172-528-2 |
| 27 | 222.5 | 14.3 | 308 | 3 | US-09-318-199-2 |

| | | | | | | |
|----|-------|------|-----|---|-------------------|-------------------|
| 28 | 222.5 | 14.3 | 308 | 3 | US-09-503-579-2 | Sequence 2, App11 |
| 29 | 218.5 | 14.1 | 432 | 2 | US-08-937-466-4 | Sequence 4, App11 |
| 30 | 218.5 | 14.1 | 432 | 2 | US-09-172-528-4 | Sequence 4, App11 |
| 31 | 218.5 | 14.1 | 432 | 3 | US-09-318-199-4 | Sequence 4, App11 |
| 32 | 218.5 | 14.1 | 432 | 3 | US-09-503-579-4 | Sequence 4, App11 |
| 33 | 208.5 | 13.4 | 293 | 4 | US-09-501-558-4 | Sequence 4, App11 |
| 34 | 196.5 | 12.7 | 307 | 2 | US-08-807-861A-56 | Sequence 56, App1 |
| 35 | 196.5 | 12.7 | 307 | 3 | US-09-210-681-56 | Sequence 56, App1 |
| 36 | 196.5 | 12.7 | 307 | 4 | US-08-946-719A-56 | Sequence 56, App1 |
| 37 | 196.5 | 12.7 | 307 | 4 | US-09-547-983-56 | Sequence 56, App1 |
| 38 | 193 | 12.4 | 303 | 1 | US-08-294-522B-36 | Sequence 36, App1 |
| 39 | 192 | 12.4 | 303 | 1 | US-08-518-878B-37 | Sequence 37, App1 |
| 40 | 192 | 12.4 | 303 | 2 | US-08-807-861A-37 | Sequence 37, App1 |
| 41 | 192 | 12.4 | 303 | 2 | US-08-470-868A-37 | Sequence 37, App1 |
| 42 | 192 | 12.4 | 303 | 3 | US-09-210-681-37 | Sequence 37, App1 |
| 43 | 192 | 12.4 | 303 | 3 | US-08-946-719A-37 | Sequence 37, App1 |
| 44 | 192 | 12.4 | 303 | 4 | US-09-547-983-37 | Sequence 37, App1 |
| 45 | 190.5 | 12.3 | 306 | 5 | PCT-US94-09799-1 | Sequence 1, App11 |

ALIGNMENTS

RESULT 1
US-09-434-354-47
Sequence 47, Application US/09434354

Patent No. 6562563
GENERAL INFORMATION:

APPLICANT: Murphy, Anne N.

APPLICANT: Cleveneger, William

APPLICANT: Wiley, Sandra Eileen

APPLICANT: Andreyev, Alexander Y.

APPLICANT: Frigeri, Luciano G.

APPLICANT: Veliceloh, Gonul

APPLICANT: Davis, Robert E.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETERMINING

TITLE OF INVENTION: INTERACTIONS OF MITOCHONDRIAL COMPONENTS, AND FOR

FILE REFERENCE: 660088.433

CURRENT APPLICATION NUMBER: US/09/434,354

CURRENT FILING DATE: 1999-11-03

NUMBER OF SEQ ID NOS: 54

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 47

LENGTH: 297

TYPE: PRT

ORGANISM: Homo sapien

US-09-434-354-47

Query Match 100.0%; Score 1553; DB 4; Length 297;

Best local Similarity 100.0%; Pred. No. 4, 2e-172; Mismatches 0; Gaps 0;

Matches 297; Conservative 0; Indels 0; Gaps 0;

| | | | | | |
|----|-----|----------------------|----|---|-----|
| QY | 1 | MGDMSFLKDFLAGAATAA | VS | KTAVAPLIERVLLQVHASKOISAEKQKGIIDCVVR | 60 |
| DB | 1 | MGDMSFLKDFLAGAATAA | VS | KTAVAPLIERVLLQVHASKOISAEKQKGIIDCVVR | 60 |
| QY | 61 | IPKEQGFSLSWKRNLANVIR | VS | PTQALNFRFKKTYQQLFLGVDYDRKQKRRYFAGNIASG | 120 |
| DB | 61 | IPKEQGFSLSWKRNLANVIR | VS | PTQALNFRFKKTYQQLFLGVDYDRKQKRRYFAGNIASG | 120 |
| QY | 121 | GAGGATSLCFVYVYLDFA | VS | RFLADVGRRAQREPHGDCITIKFSKDSGLGLQGFNVSV | 180 |
| DB | 121 | GAGGATSLCFVYVYLDFA | VS | RFLADVGRRAQREPHGDCITIKFSKDSGLGLQGFNVSV | 180 |
| QY | 181 | QGIITIRAAVFGVYDTAK | VS | GMGLPDKNVHIFVSMIAQSVYAVAGLLSYEPDYRRBMNQ | 240 |
| DB | 181 | QGIITIRAAVFGVYDTAK | VS | GMGLPDKNVHIFVSMIAQSVYAVAGLLSYEPDYRRBMNQ | 240 |
| QY | 241 | SGRRKADIWYTGVDQW | VS | RRIKAKDEGAKAFPKGMSVNLKRMGAFVLYLYDEIKKYV | 297 |
| DB | 241 | SGRRKADIWYTGVDQW | VS | RRIKAKDEGAKAFPKGMSVNLKRMGAFVLYLYDEIKKYV | 297 |

RESULT 2
US-08-961-871-10
Sequence 10, Application US/08961871
Patent No. 6013858
GENERAL INFORMATION:
APPLICANT: Wallace, Douglas C.
APPLICANT: Graham, Brett H.
APPLICANT: Macgregor, Grant R.
TITLE OF INVENTION: Mouse lacking Heart-Muscle Adenine
TITLE OF INVENTION: Nucleotide Translocator Protein and Methods
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESSES:
ADDRESSEE: Greenlee, Winner and Sullivan, P.C.
STREET: 5370 Manhattan Circle, Suite 201
CITY: Boulder
STATE: Colorado
COUNTRY: US
ZIP: 80303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,871
FILING DATE: 31-OCT-1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/030,017
FILING DATE: 01-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Feider, Donna M.
REGISTRATION NUMBER: 33,878
REFERENCE/DOCKET NUMBER: 78-96
TELEPHONE: (303) 499-8080
TELEFAX: (303) 499-8089
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 298 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-961-871-10
Query Match 93.9%; Score 1457.5; DB 3; Length 298;
Best Local Similarity 93.6%; Pred. No. 5.4e-161;
Matches 279; Conservative 10; Mismatches 8; Indels 1; Gaps 1;
QY 1 MGDHWSFLDFLAGAAVAAVSKTAAPVIERVKLLQVONASKQISAEKQYKGIIDCVR 60
DB 1 MGDALSLDFLAGIAAASKTAAPVIERVKLLQVONASKQISAEKQYKGIIDCVR 60
QY 61 IPKQGFSLFWRGLAVIRFPYQALNFAFKDKYKOLFAGVDRHGFRRYFAGNLASG 120
DB 61 IPKQGFSLFWRGLAVIRFPYQALNFAFKDKYKOLFAGVDRHGFRRYFAGNLASG 120
QY 121 GAAGATSLCFYYPIDFARTRLADVGR-RAOREFHGLGDCIIKFKSDGLKGLYQGFNV 179
DB 121 GAAGATSLCFYYPIDFARTRLADVGR-RAOREFHGLGDCIIKFKSDGLKGLYQGFNV 179
QY 180 VQGIITRAAYFEGYDPAKGLPDPKNVHIFVSMIAQSYTAVAGLSYPPDYRRMM 239
DB 180 VQGIITRAAYFEGYDPAKGLPDPKNVHIFVSMIAQSYTAVAGLSYPPDYRRMM 239
QY 181 VQGIITRAAYFEGYDPAKGLPDPKNVHIFVSMIAQSYTAVAGLSYPPDYRRMM 240
DB 181 VQGIITRAAYFEGYDPAKGLPDPKNVHIFVSMIAQSYTAVAGLSYPPDYRRMM 240
QY 240 QSGRKGADIMYTGIVDCMRKIAKDEGAKAFKFGAMSVNLGMSGAFVLYLDEIKKY 297
DB 241 QSGRKGADIMYTGIVDCMRKIAKDEGAKAFKFGAMSVNLGMSGAFVLYLDEIKKY 298
RESULT 3
US-09-434-354-48

Sequence 48, Application US/09434354
Patent No. 6562563
GENERAL INFORMATION:
APPLICANT: Murphy, Anne N.
APPLICANT: Clevenger, William
APPLICANT: Wiley, Sandra Eileen
APPLICANT: Andreyev, Alexander Y.
APPLICANT: Frigert, Luciano G.
APPLICANT: Velicelbel, Gonul
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETERMINING
TITLE OF INVENTION: INTERACTIONS OF MITOCHONDRIAL COMPONENTS, AND FOR
FILE REFERENCE: 660088.433
CURRENT APPLICATION NUMBER: US/09/434,354
CURRENT FILING DATE: 1999-11-03
NUMBER OF SEQ ID NOS: 54
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 48
LENGTH: 298
TYPE: PRT
ORGANISM: Homo sapien
US-09-434-354-48
Query Match 89.6%; Score 1391.5; DB 4; Length 298;
Best Local Similarity 88.6%; Pred. No. 2.5e-153;
Matches 263; Conservative 17; Mismatches 16; Indels 1; Gaps 1;
QY 1 MGDHWSFLDFLAGAAVAAVSKTAAPVIERVKLLQVONASKQISAEKQYKGIIDCVR 60
DB 1 MTDALSPFADFLAGVAAVSKTAAPVIERVKLLQVONASKQITADKQYKGIIDCVR 60
QY 61 IPKQGFSLFWRGLAVIRFPYQALNFAFKDKYKOLFAGVDRHGFRRYFAGNLASG 120
DB 61 IPKQGFSLFWRGLAVIRFPYQALNFAFKDKYKOLFAGVDRHGFRRYFAGNLASG 120
QY 121 GAAGATSLCFYYPIDFARTRLADVGR-RAOREFHGLGDCIIKFKSDGLKGLYQGFNV 179
DB 121 GAAGATSLCFYYPIDFARTRLADVGR-RAOREFHGLGDCIIKFKSDGLKGLYQGFNV 179
QY 180 VQGIITRAAYFEGYDPAKGLPDPKNVHIFVSMIAQSYTAVAGLSYPPDYRRMM 239
DB 180 VQGIITRAAYFEGYDPAKGLPDPKNVHIFVSMIAQSYTAVAGLSYPPDYRRMM 239
QY 240 QSGRKGADIMYTGIVDCMRKIAKDEGAKAFKFGAMSVNLGMSGAFVLYLDEIKKY 296
DB 241 QSGRKGADIMYTGIVDCMRKIAKDEGAKAFKFGAMSVNLGMSGAFVLYLDEIKKY 297
RESULT 4
US-09-434-354-49
Sequence 49, Application US/09434354
Patent No. 6562563
GENERAL INFORMATION:
APPLICANT: Murphy, Anne N.
APPLICANT: Clevenger, William
APPLICANT: Wiley, Sandra Eileen
APPLICANT: Andreyev, Alexander Y.
APPLICANT: Frigert, Luciano G.
APPLICANT: Velicelbel, Gonul
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETERMINING
TITLE OF INVENTION: INTERACTIONS OF MITOCHONDRIAL COMPONENTS, AND FOR
FILE REFERENCE: 660088.433
CURRENT APPLICATION NUMBER: US/09/434,354
CURRENT FILING DATE: 1999-11-03
NUMBER OF SEQ ID NOS: 54
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 49
LENGTH: 298
TYPE: PRT
ORGANISM: Homo sapien

US-09-434-354-49

Query Match 89.2%; Score 1385.5; DB 4; Length 298;
Best Local Similarity 87.2%; Pred. No. 1,3e-152;
Matches 260; Conservative 21; Mismatches 16; Indels 1; Gaps 1;

QY 1 MGDHMSFLKPLFGAANAASKTAAPAEIERVKLLLOVHASKOISAEKOKGIIIDCYR 60
1 MTEQAIISFANKDFLGGIAAIAKTAAPAEIERVKLLLOVHASKOIAADKOKYGIYDCIVR 60
QY 61 IPKGGFSPFWRGNLANIYRFPQALNFAFKDKYKOLFSGVDRHKGFWYFPGNLSG 120
61 IPKGGFSPFWRGNLANIYRFPQALNFAFKDKYKOLFSGVDRHKGFWYFPGNLSG 120
QY 121 GAAGATSLCFEYPLDFARTRLADYGR-AQREFHGLDCLIKIFKSDGLNGLYGFVNS 179
121 GAAGATSLCFEYPLDFARTRLADYGR-AQREFHGLDCLIKIFKSDGLNGLYGFVNS 180
QY 180 VGGIITIAAFGYITDFAKGLPDPKNVHIFVSMIAOSVAVAGLSYPTDYRRMM 239
181 VGGIITIAAFGYITDFAKGLPDPKNVHIFVSMIAOSVAVAGLSYPTDYRRMM 240
QY 240 QSGRGADIMYTGIVDCRKIAKDEGAKAFKGAAMNVLKMGAFVLVDEIKKYV 297
241 QSGRGADIMYTGIVDCRKIAKDEGAKAFKGAAMNVLKMGAFVLVDEIKKYV 298
Db

RESULT 5

US-09-996-243-289

Sequence 289, Application US/09996243

Patent No. 6478825

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.
APPLICANT: Baker, Kevin P.
APPLICANT: Borstein, David
APPLICANT: Desnoyers, Luc
APPLICANT: Eaton, Dan L.
APPLICANT: Ferrara, Napoleone
APPLICANT: Fong, Sherman
APPLICANT: Gerber, Hanspeter E.
APPLICANT: Gottard, Audrey
APPLICANT: Godowski, Paul J.
APPLICANT: Grimaldi, J. Christopher
APPLICANT: Gurney, Austin L.
APPLICANT: Kljavin, Ivar J.
APPLICANT: Napier, Mary A.
APPLICANT: Paol, James
APPLICANT: Paol, Nicholas F.
APPLICANT: Roy, Margaret Ann
APPLICANT: Stewart, Timothy A.
APPLICANT: Tumas, Daniel
APPLICANT: Watanabe, Colin K.
APPLICANT: Williams, P. Mickey
APPLICANT: Wood, William I.
APPLICANT: Zhang, Zhenli
TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic
FILE REFERENCE: P2730P1C13
CURRENT FILING DATE: US/09/996,243
CURRENT FILING DATE: 2001-11-14
PRIOR APPLICATION NUMBER: 60/049787
PRIOR FILING DATE: 1997-06-16
PRIOR APPLICATION NUMBER: 60/062250
PRIOR FILING DATE: 1997-10-17
PRIOR APPLICATION NUMBER: 60/065186
PRIOR FILING DATE: 1997-11-12
PRIOR APPLICATION NUMBER: 60/065311
PRIOR FILING DATE: 1997-11-13
PRIOR APPLICATION NUMBER: 60/066770
PRIOR FILING DATE: 1997-11-24
PRIOR APPLICATION NUMBER: 60/075945
PRIOR FILING DATE: 1998-02-25

PRIOR APPLICATION NUMBER: 60/078910
PRIOR FILING DATE: 1998-03-20
PRIOR APPLICATION NUMBER: 60/083322
PRIOR FILING DATE: 1998-04-28
PRIOR APPLICATION NUMBER: 60/084600
PRIOR FILING DATE: 1998-05-07
PRIOR APPLICATION NUMBER: 60/087106
PRIOR FILING DATE: 1998-05-28
PRIOR APPLICATION NUMBER: 60/087607
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087609
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087759
PRIOR FILING DATE: 1998-06-02
PRIOR APPLICATION NUMBER: 60/087827
PRIOR FILING DATE: 1998-06-03
PRIOR APPLICATION NUMBER: 60/088021
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088025
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088026
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088028
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088029
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088030
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088033
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088326
PRIOR FILING DATE: 1998-06-04
PRIOR APPLICATION NUMBER: 60/088167
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088202
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088212
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088217
PRIOR FILING DATE: 1998-06-05
PRIOR APPLICATION NUMBER: 60/088655
PRIOR FILING DATE: 1998-06-09
PRIOR APPLICATION NUMBER: 60/088734
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088738
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088742
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088810
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088824
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088826
PRIOR FILING DATE: 1998-06-10
PRIOR APPLICATION NUMBER: 60/088858
PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/088861
PRIOR FILING DATE: 1998-06-11
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PRIOR FILING DATE: 1998-06-11
PRIOR APPLICATION NUMBER: 60/089105
PRIOR FILING DATE: 1998-06-12
PRIOR APPLICATION NUMBER: 60/089440
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089512
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089514
PRIOR FILING DATE: 1998-06-16
PRIOR APPLICATION NUMBER: 60/089532
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089538
PRIOR FILING DATE: 1998-06-17
PRIOR APPLICATION NUMBER: 60/089598

| | | | |
|----|-----|---|-----|
| Db | 234 | IREGGAKSLMNGNINVLKIAPEKSIKFMAYEQMKRLV--GSDQETLRIRHER----- | 283 |
| Qy | 117 | LASGAGATSLCEPYPLDFAFTRLAADVGRAQDEEFGHCICIKIFESDGLRGLYQGE | 176 |
| Db | 284 | LAAGSLALAIKSSITYPEMVELKTRNAL----RKTQYSGMDLCARRILAKEGVAAPFYKY | 339 |
| Qy | 177 | NVVOGIIITYRAAYGVYDFAKGM-----LPDPKNVHIFVSNWIAQSYATAVAG-LIS | 227 |
| Db | 340 | IPNNLGIIPYAGIDLAIVETIKNTLQRYAVNSADP---GVYV-LIACGTTISSTGQLMS | 395 |
| Qy | 228 | YPEDTVRRMMQSGRKGADIMYTGTVDQWRKRIANDEGAKAFEFKGSNVLRGMGAFY- | 286 |
| Db | 396 | YPLALVTRFMQAOASIEGAPETWSSL--FKQILRTGCAFGLYRGIAHPNFMKVIYPAVSIS | 453 |
| Qy | 287 | LVLADLRK | 294 |
| Db | 454 | YVVTENLR | 461 |

```

0001  RESULT 7
0002  US-09-312-283C-339
0003  : Sequence 339, Application US/09312283C
0004  : Patent No. 6573055
0005  :
0006  : GENERAL INFORMATION:
0007  :
0008  : APPLICANT: Watson, James D.
0009  : APPLICANT: Strachan, Lorna
0010  : APPLICANT: Sleeman, Matthew
0011  : APPLICANT: Onrust, Rene
0012  : APPLICANT: Murison, James G.
0013  : APPLICANT: Kumble, Krishanand D.
0014  :
0015  : TITLE OF INVENTION: Compositions Isolated from Skin Cells
0016  :
0017  : TITLE OF INVENTION: and Methods for Their Use
0018  :
0019  : FILE REFERENCE: 11000-1011c2
0020  :
0021  : CURRENT APPLICATION NUMBER: US/09/312,283C
0022  :
0023  : CURRENT FILING DATE: 1999-05-14
0024  :
0025  : NUMBER OF SEQ ID NOS: 425
0026  :
0027  : SOFTWARE: FastSeq for Windows Version 4.0
0028  :
0029  : SEQ ID NO 339
0030  :
0031  : LENGTH: 469
0032  :
0033  : TYPE: PRF
0034  :
0035  : ORGANISM: Mouse
0036  :
0037  : US-09-312-283C-339

```

| | | | | |
|-----------------------|--------|------------------|--------|-----------------|
| Query Match | 19.4%; | Score 301; | DB 4; | Length 469; |
| Best Local Similarity | 28.9%; | Pred. No. 3e-26; | | |
| Matches | 89; | Conservative | 64; | Mismatches 103; |
| | | | Indels | 52; |
| | | | Gaps | 14; |

```

OY      6 MSFLKEDFLAGAAVAASVTAAPVPIRRVKLLLOVOHAKROISAEKOYGLIIDCV-----RI 61
Dd      187 WRHL---VAGSGAGAVSRCTCAPLDRLKALMOY-HASBRNNM-----CLVGGETOM 233

OY      62 PKREGELSFWRGNLANVIRYPTQALNFAEKDKYOLETLAGVDYR-----HKOFWRYPAGN 116
Dd      234 IREGGAKMLRWNGINVLTKIAPESAIKFMAVQOMRKLV--GSDOETLRITHER----- 283

OY      117 LASGAAGAATSLCFEYPLDEPARTLAADVGRARQRFHGIDPICIIKFPSDGLRGLYOGF 176
Dd      284 LVAGSLAALANOSTSYIPHEVLKTRMAL-----KTGGYSMDLCARRIILKEGVAAALYYKY 339

OY      177 NVSVQGIIITYRAIFYGYDTAKGM-----LPBPKNVHIIFYSMIAOSVTAAVAC-LLS 227
Dd      340 IPNMIGIILPYAGIDLAVYEYLKNTWLORYAVNSADP--GVFPV-LIACGISISTCOLAS 395

OY      228 YPFEDIVRRMMQMSGRKKADIMXTGTVDQCWRKIARDEGAKAFEGAMSNVLRMGAFV- 286
Dd      396 YPLALVFRRMQAQSIEGAPEVYTMSSL-FKQILNRREGANGFLYRGLIAPNPMKVIIPAVIS 453

OY      287 LVLHYDEIK 294
Dd      454 YVVEENLK 461

```

RESULT 8

```

US-09-160-119-4
? Sequence 4, Application US/09160119A
? Patent No. 6316219
? GENERAL INFORMATION:
? APPLICANT: KRIEF, STEPHANE
? APPLICANT: SODICHER, MICHEL
? APPLICANT: BRIL, ANTOINE
? TITLE OF INVENTION: NOVEL COMPOUNDS
? FILE REFERENCE: GH-30985
? CURRENT APPLICATION NUMBER: US/09/160,119A
? EARLIER FILING DATE: 1998-09-24
? EARLIER APPLICATION NUMBER: EP 97402511.6
? EARLIER FILING DATE: 1997-10-23
? EARLIER APPLICATION NUMBER: EP 98401655.0
? EARLIER FILING DATE: 1998-07-02
? NUMBER OF SEQ ID NOS: 4
? SOFTWARE: FastSeq for Windows Version 3.0
? SEQ ID NO 4
? LENGTH: 447
? TYPE: prt
? ORGANISM: HOMO SAPIENS
US-09-160-119-4

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Query Match 18.7%; Score 291; DB 4; Length 447;
Best Local Similarity-27.5%; Pred. No. 4.1e-25;
Matches 80; Conservative 53; Mismatches 136; Indels 22; Gaps 7;

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OY 12 LAGVAAAVASTAAVAFIERVYLLLOVOHSAKSIASEKQYKGIIDCVVIRPKQGLSPM 71
   | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : |
Db 104 FGLSSVAGAVGNTANYPIDLVYTRQNRQNSSTGSPFGLMAYKNSFDFCKRYLREGFFGLX 163
   | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : |
OY 72 RGNLANVIRYPTQALNFAFKDKYQLEFYGVDYRHKQWRYRAGNINLASGGAAGATSLCEV 131
   | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : |
Db 164 RGLLPOLLGVAVEKAIKLTVNDFVDRKEM----HKDGSVPLAAEILAGCAGGSOVIFT 218
   | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : |
OY 132 YPLDFAPTRL--AAAV--GRAQRREHGLGDICIKFKSDGLGKLOGEFNVNSQOGLIYR 187
   | : | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : |
Db 219 NFLEIVYKIRLOVAGEITTGSPRVS-----ALSIVYRDLGFGGIYKGAACPLRDIPPS 269
   | : | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : |
OY 188 AAYFVGYDTAKGMELDPKNVHLFVSMMIAOSTYAV--AGLLSYPTDVRRRMMMOGRKGA 246
   | | | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : |
Db 270 AAYFPCYAHVKASFANEDQVSPGSLILLAGALAGMAPASLVPADVIKTR--LQVAARAG 327
   | | | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : |
OY 247 DIMYGYVDQWRKIAKDEGAKAFPFGGAMSNVLRGMGG--AFVLYVYDEIKKY 296
   | : | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : |
Db 328 QTTYSGVYIDCEFKILIREEGPKALMGAGARVRSSDFQGVYLLTLYLLLRW 378
   | : | : | | : | | : | | : | | : | | : | | : | | : | | : | | : | | : |

```

```

1  RESULT 9
2  US-09-160-119-2
3  : Sequence 2, Application US/09160119A
4  : Patent No. 6316219
5  : GENERAL INFORMATION:
6  : APPLICANT: KRIEF, STEPHANE
7  : APPLICANT: SODCHET, MICHEL
8  : APPLICANT: BRIL, ANTOINE
9  : TITLE OF INVENTION: NOVEL COMPOUNDS
10 : FILE REFERENCE: GH-30985
11 : CURRENT APPLICATION NUMBER: US/09/160,119A
12 : CURRENT FILING DATE: 1998-09-24
13 : EARLIER APPLICATION NUMBER: EP 97402511.6
14 : EARLIER FILING DATE: 1997-10-23
15 : EARLIER APPLICATION NUMBER: EP 98401655.0
16 : EARLIER FILING DATE: 1998-07-02
17 : NUMBER OF SEQ ID NOS: 4
18 : SOFTWARE: FastSeq for Windows Version 3.0
19 : SEQ ID NO 2
20 : LENGTH: 674
21 : TYPE: PRT
22 : ORGANISM: HOMO SAPIENS
23 : US-09-160-119-2

```

Query Match 18.7%; Score 291; DB 4; Length 674;

[illegible]

```

RESULT 10
US-09-501-558-2
: Sequence 2, Application US/09501558
: Patent No. 6403784
: GENERAL INFORMATION:
: APPLICANT: Turner, C. Alexander Jr.
: APPLICANT: Mathur, Brian
: APPLICANT: Zambrowicz, Brian
: APPLICANT: Sands, Arthur T.
: TITLE OF INVENTION: No. 6403784el Human Uncoupling Proteins and
: TITLE OF INVENTION: Polynucleotides Encoding the Same
: FILE REFERENCE: LEX-0012-USA
: CURRENT APPLICATION NUMBER: US/09/501,558
: CURRENT FILING DATE: 2000-02-09
: NUMBER OF SEQ ID NOS: 4
: SOFTWARE: FastSeq for Windows Version 3.0
: SEQ ID NO 2
: LENGTH: 291
: TYPE: prt
: ORGANISM: Homo sapiens
: US-09-501-558-2

```

| | | | | |
|-----------------------|------------------|--------------------|------------|-------------|
| Query Match | 17.2% | Score 267; | DB 4; | Length 291; |
| Best Local Similarity | 28.4% | Pred. No. 1.3e-22; | | |
| Matches 84; | Conservative 51; | Mismatches 137; | Indels 24; | Gaps 9 |

```

Oy      10 KDLGAGVAAASAKTVAAIERKFKLLQVQASNOIS-AEKQKIIDCVYIRPEQGL 68
      11 | : : : : : | : : : : : | : : : : : | : : : : : |
Db      7 KPPVYGAGLSITAECSCTFPIDILKTRLRQOGSTNARKKEIYRKMHLAIVIRREGSK 66

Oy      69 SFNRGLNVIYRIEPPQALNFAFKDKYKOLETGVGDHKKQFWRYPAGMLASGAAGATSL 128
      10 | : : : : : | : : : : : | : : : : : | : : : : : |
Db      67 ALYSGIAPMALRQASVYTIKIGTYSOKLFL--IEREPD--ETLPVIVIGILSGVISS 121

Oy      129 CFYVPIDFARTPLAAVYVGRRAOREPHGLADCIIRKFDGSLRGVQGFNVSVQGIITYRA 188
      10 | : : : : : | : : : : : | : : : : : | : : : : : |
Db      122 TINPFDVLKIRKQA-----QSNITIGAGMGFNMTIYQDEBTRGMLKGVSLTAQRAALVYG 177

Oy      189 AYFGVYDTAK-----GMLPDRKNVHIEVSMIAQSVTAVAG-LISYFDTVRRMMQOS 241
      11 | : : : : : | : : : : : | : : : : : | : : : : : |
Db      178 VELPVPYDITKKHLILSLGMLGDPVYTHFLSSF-----TCGLGALASINVPDVVFTRMNOR 232

Oy      242 G-BKRGADIMYTGVDQCMRIARDEGAKKAFKAGMSNVLR-OMGAGFVLYLTDEKIK 295
      11 | : : : : : | : : : : : | : : : : : | : : : : : |
Db      233 VLWDGRCSGTGTGVLDELDTQMKRNEGFAFKCFPMNMLRLGPMNIIFFVYEQULK 288

```

RESULT 11
US-09-482-273-118

```

Sequence 118, Application US/09482273
Patent No. 6534631

GENERAL INFORMATION:
APPLICANT: Rosen et al.
TITLE OF INVENTION: 71 Human Secreted Proteins
FILE REFERENCE: P203001
CURRENT APPLICATION NUMBER: US/09/482, 273
CURRENT FILING DATE: 2000-01-13
EARLIER APPLICATION NUMBER: PCT/US99/15849
EARLIER FILING DATE: 1999-07-14
EARLIER APPLICATION NUMBER: 60/092, 921
EARLIER FILING DATE: 1998-07-15
EARLIER APPLICATION NUMBER: 60/092, 922
EARLIER FILING DATE: 1998-07-15
EARLIER APPLICATION NUMBER: 60/092, 956
EARLIER FILING DATE: 1998-07-15
NUMBER OF SEQ ID NOS: 267
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 118
LENGTH: 335
TYPE: PRT
ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: SITE
LOCATION: (335)
OTHER INFORMATION: xaa equals stop translation
US-09-482-273-118

```

| | | | | |
|-----------------------|-------|-------------------|----------------|------------|
| Query Match | 17.1% | Score 265.5 | DB 4 | Length 335 |
| Best Local Similarity | 30.0% | Pred. NO. 2.4e-22 | | |
| Matches | 89 | Conservative 43 | Mismatches 136 | Indels 27 |
| | | | | Gaps 10 |

RESULT 12
 US-08-933-750C-12
 : Sequence 12, Application US/08933750C
 : Patient No 5937442
 :
 : GENERAL INFORMATION:
 :
 : APPLICANT: Lal, Preeti
 : APPLICANT: Hillman, Jennifer L.
 : APPLICANT: Bandman, Olga
 : APPLICANT: Shah, Purvi
 : APPLICANT: Au-Young, Janice
 : APPLICANT: Yue, Henry
 : APPLICANT: Guebler, Karl J.
 : APPLICANT: Corley, Neil C.
 : TITLE OF INVENTION: HUMAN REGULATORY MOLECULES
 : NUMBER OF SEQUENCES: 98
 :
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Incyte Pharmaceuticals, Inc.
 : STREET: 3174 Porter Drive
 : CITY: Palo Alto
 : STATE: CA

COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/933,750C
FILING DATE: September 23, 1997
CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0356 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 320 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: SPLN00702
CLONE: 207452
US-08-933-750C-12

Query Match 15.3%; Score 238; DB 2; Length 320;
Best Local Similarity 23.5%; Pred. No. 3.6e-19;
Matches 71; Conservative 67; Mismatches 124; Indels 40; Gaps 10;

QY 13 LAGAVAAVSKTAAVPIERVKLLQVOHAS-KQISAERQYKGIIDCVIRIPKEQGLSEFW 71
DB 20 VAGSVGLVTRALISPFVQIKIRFQLOHERLSRSDPSAKYHGIIQASROIQEEGPTAFW 79
QY 72 RGNLANVIRYPTQALNF-AFKDKYKQLEFGVDHKKQFWRFAGNLASGGAAGTSLCF 130
DB 80 KGHVPAQILISIGYAVOPLSEFMLETLVHSGSVYDAREFSVHF---VCGGLAACMATLT 135
QY 131 VYPLDFARTRLAADVGRRAQREHGLGDCIIKIFKSDLRGLGYGFNVSVQGIITRYRAY 190
DB 136 VHPVDVLTFRFA---QGEPRYVNTLRHVAVGMYRSEBPQYFKGLAPTLIAIFPYAGIQ 192
QY 191 FGVDYTAAGMLPDPKNNHIEVSWMT-----AOSVTAAGLSTYPPDVYR 235
DB 193 FSCYSLSLK-----HLV-KWAIIPAEGKKNNENQNLCSGAGVISTKLTLYPDLFRK 242
QY 236 RMM---OSGRK--GADIMYGTVDQWCKRIADDEGAKAFKFGAMSNVLR-GMGAFVLYL 289
DB 243 RLQVCGFEHARAFAQVRRYKGLMDCAKQVLOKEGALFEFGKLSPLKALSTGFMEFS 302
QY 290 YD 291
DB 303 YE 304

RESULT 13
US-09-234-613-12
Sequence 12, Application US/09234613
Patent No. 6132973
GENERAL INFORMATION:
APPLICANT: Lal, Preeti
APPLICANT: Hillman, Jennifer L.
APPLICANT: Bandman, Olga
APPLICANT: Shah, Purvi
APPLICANT: Au-Yang, Janice
APPLICANT: Yue, Henry

APPLICANT: Guegler, Karl J.
APPLICANT: Corley, Neil C.
TITLE OF INVENTION: HUMAN REGULATORY MOLECULES
NUMBER OF SEQUENCES: 98
CORRESPONDENCE ADDRESS:
ADDRESSEE: Incyte Pharmaceuticals, Inc.
STREET: 3174 Porter Drive
CITY: Palo Alto
STATE: CA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/234,613
FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/933,750
FILING DATE: September 23, 1997
ATTORNEY/AGENT INFORMATION:
NAME: Billings, Lucy J.
REGISTRATION NUMBER: 36,749
REFERENCE/DOCKET NUMBER: PF-0356 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-855-0555
TELEFAX: 415-845-4166
TELEX:
INFORMATION FOR SEQ ID NO: 12:
SEQUENCE CHARACTERISTICS:
LENGTH: 320 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
LIBRARY: SPLN00702
CLONE: 207452
US-09-234-613-12

Query Match 15.3%; Score 238; DB 3; Length 320;
Best Local Similarity 23.5%; Pred. No. 3.6e-19;
Matches 71; Conservative 67; Mismatches 124; Indels 40; Gaps 10;

QY 13 LAGAVAAVSKTAAVPIERVKLLQVOHAS-KQISAERQYKGIIDCVIRIPKEQGLSEFW 71
DB 20 VAGSVGLVTRALISPFVQIKIRFQLOHERLSRSDPSAKYHGIIQASROIQEEGPTAFW 79
QY 72 RGNLANVIRYPTQALNF-AFKDKYKQLEFGVDHKKQFWRFAGNLASGGAAGTSLCF 130
DB 80 KGHVPAQILISIGYAVOPLSEFMLETLVHSGSVYDAREFSVHF---VCGGLAACMATLT 135
QY 131 VYPLDFARTRLAADVGRRAQREHGLGDCIIKIFKSDLRGLGYGFNVSVQGIITRYRAY 190
DB 136 VHPVDVLTFRFA---QGEPRYVNTLRHVAVGMYRSEBPQYFKGLAPTLIAIFPYAGIQ 192
QY 191 FGVDYTAAGMLPDPKNNHIEVSWMT-----AOSVTAAGLSTYPPDVYR 235
DB 193 FSCYSLSLK-----HLV-KWAIIPAEGKKNNENQNLCSGAGVISTKLTLYPDLFRK 242
QY 236 RMM---OSGRK--GADIMYGTVDQWCKRIADDEGAKAFKFGAMSNVLR-GMGAFVLYL 289
DB 243 RLQVCGFEHARAFAQVRRYKGLMDCAKQVLOKEGALFEFGKLSPLKALSTGFMEFS 302
QY 290 YD 291
DB 303 YE 304

RESULT 14
US-09-142-565-2

GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 28, 2003, 19:38:56 ; Search time 19.29 Seconds

(without alignments)
2105.969 Million cell updates/sec

Title: US-09-811-132-31

Perfect score: 1553
Sequence: 1 MGDHMSFLKDFLAGAATAA.....LRGNGAFVLYDEIRKRV 297

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 510680 seqs, 136781880 residues

Total number of hits satisfying chosen parameters: 510680

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published_Applications_AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/1/pubpaa/PTI_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
- 6: /cgn2_6/ptodata/1/pubpaa/PTIUS_PUBCOMB.pep:*
- 7: /cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
- 8: /cgn2_6/ptodata/1/pubpaa/US08_PUBCOMB.pep:*
- 9: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
- 10: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/1/pubpaa/US09_NEW_PUB.pep:*
- 13: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep:*
- 17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
- 18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|--------|-------------|--------|-------|--------------------|
| 1 | 1553 | 100.0 | 297 | 9 | US-09-811-094-31 |
| 2 | 1553 | 100.0 | 297 | 9 | US-09-810-644-31 |
| 3 | 1553 | 100.0 | 297 | 10 | US-09-185-904A-31 |
| 4 | 1391.5 | 89.6 | 298 | 9 | US-09-811-094-32 |
| 5 | 1391.5 | 89.6 | 298 | 9 | US-09-810-644-32 |
| 6 | 1391.5 | 89.6 | 298 | 10 | US-09-185-904A-32 |
| 7 | 1385.5 | 89.2 | 298 | 9 | US-09-811-094-33 |
| 8 | 1385.5 | 89.2 | 298 | 9 | US-09-810-644-33 |
| 9 | 1385.5 | 89.2 | 298 | 10 | US-09-185-904A-33 |
| 10 | 740 | 47.6 | 381 | 12 | US-10-141-478A-2 |
| 11 | 734 | 47.3 | 318 | 10 | US-09-801-368-252 |
| 12 | 734 | 47.3 | 386 | 9 | US-09-734-569-110 |
| 13 | 703.5 | 45.3 | 308 | 15 | US-10-128-714-3338 |
| 14 | 703.5 | 45.3 | 308 | 15 | US-10-128-714-8338 |
| 15 | 666 | 42.9 | 677 | 12 | US-10-259-165-192 |

| | | | | | | |
|----|-------|------|-----|----|---------------------|--------------------|
| 16 | 461 | 29.7 | 132 | 9 | US-09-925-301-1459 | Sequence 1459, App |
| 17 | 402.5 | 25.9 | 87 | 9 | US-09-864-761-36440 | Sequence 36440, A |
| 18 | 350.5 | 22.6 | 475 | 10 | US-09-777-921A-4 | Sequence 4, Appl1 |
| 19 | 346.5 | 22.3 | 477 | 10 | US-09-777-921A-2 | Sequence 2, Appl1 |
| 20 | 312 | 20.1 | 410 | 10 | US-09-777-921A-5 | Sequence 3, Appl1 |
| 21 | 304 | 19.6 | 469 | 9 | US-09-989-722-289 | Sequence 289, App |
| 22 | 304 | 19.6 | 469 | 9 | US-09-989-723-289 | Sequence 289, App |
| 23 | 304 | 19.6 | 469 | 9 | US-09-989-729-289 | Sequence 289, App |
| 24 | 304 | 19.6 | 469 | 9 | US-09-989-727-289 | Sequence 289, App |
| 25 | 304 | 19.6 | 469 | 10 | US-09-989-731-289 | Sequence 289, App |
| 26 | 304 | 19.6 | 469 | 10 | US-09-989-732-289 | Sequence 289, App |
| 27 | 304 | 19.6 | 469 | 10 | US-09-991-073-289 | Sequence 289, App |
| 28 | 304 | 19.6 | 469 | 10 | US-09-990-442-289 | Sequence 289, App |
| 29 | 304 | 19.6 | 469 | 10 | US-09-991-163-289 | Sequence 289, App |
| 30 | 304 | 19.6 | 469 | 10 | US-09-993-604-289 | Sequence 289, App |
| 31 | 304 | 19.6 | 469 | 10 | US-09-993-604-289 | Sequence 289, App |
| 32 | 304 | 19.6 | 469 | 10 | US-09-989-721-289 | Sequence 289, App |
| 33 | 304 | 19.6 | 469 | 10 | US-09-992-578-289 | Sequence 289, App |
| 34 | 304 | 19.6 | 469 | 10 | US-09-989-293A-289 | Sequence 289, App |
| 35 | 304 | 19.6 | 469 | 10 | US-09-989-735-289 | Sequence 289, App |
| 36 | 304 | 19.6 | 469 | 10 | US-09-990-444-289 | Sequence 289, App |
| 37 | 304 | 19.6 | 469 | 10 | US-09-991-181-289 | Sequence 289, App |
| 38 | 304 | 19.6 | 469 | 10 | US-09-989-730-289 | Sequence 289, App |
| 39 | 304 | 19.6 | 469 | 10 | US-09-990-436-289 | Sequence 289, App |
| 40 | 304 | 19.6 | 469 | 10 | US-09-993-687-289 | Sequence 289, App |
| 41 | 304 | 19.6 | 469 | 11 | US-09-989-734-289 | Sequence 289, App |
| 42 | 304 | 19.6 | 469 | 11 | US-09-997-653-289 | Sequence 289, App |
| 43 | 304 | 19.6 | 469 | 11 | US-09-993-667-289 | Sequence 289, App |
| 44 | 304 | 19.6 | 469 | 11 | US-09-997-428-289 | Sequence 289, App |
| 45 | 304 | 19.6 | 469 | 11 | US-09-997-666-289 | Sequence 289, App |

ALIGNMENTS

```

RESULT 1
US-09-811-094-31
; Sequence 31, Application US/09811094
; Patent No. US20010044144A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, Christen M.
; APPLICANT: Davis, Robert E.
; APPLICANT: Clevenger, William
; APPLICANT: Wiley, Sandra Eileen
; APPLICANT: Willet, Scott W.
; APPLICANT: Szabo, Thomas R.
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Moos, Walter H.
; TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLATOR (ANT),
; FILE REFERENCE: 660088.420D4
; CURRENT APPLICATION NUMBER: US/09/811,094
; CURRENT FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 31
; LENGTH: 297
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-811-094-31
Query Match      100.0%  Score 1553; DB 9; Length 297;
Best Local Similarity 100.0%; Pred. No. 1.3e-160;
Matches 297; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
1 MGDHMSFLKDFLAGAATAAASKTAVAPIERKLLIQVHASKQISAERKGIIDCYVR 60
|||||
1 MGDHMSFLKDFLAGAATAAASKTAVAPIERKLLIQVHASKQISAERKGIIDCYVR 60
|||||
1 IKKEGFLSFWGNLANVIRFPQALNFAFDKTKQLFLGVDNRHKKQFWRFAGNLSAG 120
|||||
61 IKKEGFLSFWGNLANVIRFPQALNFAFDKTKQLFLGVDNRHKKQFWRFAGNLSAG 120
|||||
61 IKKEGFLSFWGNLANVIRFPQALNFAFDKTKQLFLGVDNRHKKQFWRFAGNLSAG 120
|||||

```

| | | | |
|----|-----|--|-----|
| Oy | 121 | GAAGATGTCVYVYELDPARFLAADVGRRAQREHGLGCCIIRKIPFSDGLRGLYOGFNVS | 180 |
| | | | |
| Db | 121 | GAAGATSLCIVYVYELDPARFLAADVGRRAQREHGLGCCIIRKIPFSDGLRGLYOGFNVS | 180 |
| Oy | 181 | OGIITIRAAVFGVYDTAKMLPDPKNVHLEFSWMLAQSVAFLSYPEFDVRRMMQ | 240 |
| | | | |
| Db | 181 | OGIITIRAAVFGVYDTAKMLPDPKNVHLEFSWMLAQSVAFLSYPEFDVRRMMQ | 240 |
| Oy | 241 | SGRGKADIWYGVQDQWRKIADDEGAKAFKCAWSNVLRGGAFLVLYVETIRKY | 297 |
| | | | |
| Db | 241 | SGRGKADIWYGVQDQWRKIADDEGAKAFKCAWSNVLRGGAFLVLYVETIRKY | 297 |

RESULT 2
 US-09-810-644-31
 : Sequence 31, Application US/09810644
 : Patent No. US20020012892A1
 :

RESULT 2
 US-09-810-644-31
 : Sequence 31. Application US/09810644
 : Patent No. US20020012992A1
 :
 : GENERAL INFORMATION:
 :
 : APPLICANT: Anderson, Christen M.
 : APPLICANT: Davis, Robert E.
 : APPLICANT: Clevenger, William
 : APPLICANT: Wiley, Sandra Ellen
 : APPLICANT: Miller, Scott W.
 : APPLICANT: Szabo, Tomas R.
 : APPLICANT: Ghosh, Soumitra S.
 : APPLICANT: Moos, Walter H.
 : APPLICANT: Pei, Yazhong
 :
 : TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT)
 : FILE REFERENCE: 660098.42003
 : CURRENT APPLICATION NUMBER: US/09/810,644
 : CURRENT FILING DATE: 2001-03-14
 : NUMBER OF SEQ ID NOS: 37
 : SOFTWARE: FastSeq for Windows Version 3.0
 :
 : SEQ ID NO 31
 : LENGTH: 297
 :
 : TYPE: PRT
 : ORGANISM: Homo sapien
 :
 : US-09-810-644-31

| | Query Match | Best Local Similarity | 100.0% ; Score 1553 ; DB 9 ; Length 297 ; |
|----|---------------|--|---|
| | Matches 297 ; | Conservative 0 ; Mismatches 0 ; Indels 0 | Pred. No. 1,3e-160 ; |
| QY | 1 | MGHANSFLKDFLAGVAAAASVKTAVAPLERKLLLOVQHASKOISAEKQTKGIIIDCVR | 60 |
| Db | 1 | MGHANSFLKDFLAGVAAAASVKTAVAPLERKLLLOVQHASKOISAEKQTKGIIIDCVR | 60 |
| QY | 61 | IPKEQGLSEWRGNLANVIRYEPPTALNFAEDKQKQJLFGVDRHQAQFMYEFAGNLASG | 120 |
| Db | 61 | IPKEQGLSEWRGNLANVIRYEPPTALNFAEDKQKQJLFGVDRHQAQFMYEFAGNLASG | 120 |
| QY | 121 | GAAGATSLCFYVPLDPARTRLAADVGRRAQREFFHGLDCLTIKFKSGLKGLYQGFVAVSY | 180 |
| Db | 121 | GAAGATSLCFYVPLDPARTRLAADVGRRAQREFFHGLDCLTIKFKSGLKGLYQGFVAVSY | 180 |
| QY | 181 | QGIIIRAAVFCVYDTAKMLDPKPNVHIFVSWMLAQSVTAAGLLSYEPEDYRRRMMQ | 240 |
| Db | 181 | QGIIIRAAVFCVYDTAKMLDPKPNVHIFVSWMLAQSVTAAGLLSYEPEDYRRRMMQ | 240 |
| QY | 241 | SGRRKGADIMTGVQVOCMKRIADDEAKKAFFGAMSNNVLRGGAGFVLYLDELIRKYY | 297 |
| Db | 241 | SGRRKGADIMTGVQVOCMKRIADDEAKKAFFGAMSNNVLRGGAGFVLYLDELIRKYY | 297 |

RESULT 3
US-09-185-904A-31
Sequence 31, Application US/09185904A
Patent No. US20020177165A1
GENERAL INFORMATION:
APPLICANT: Anderson, Christen M.
APPLICANT: Davis, Robert E.

```

1  APPLICANT: Cleveland, William
2  APPLICANT: Wiley, Sandra Eileen
3  APPLICANT: Miller, Scott W.
4  APPLICANT: Szabo, Tomas R.
5  APPLICANT: Ghosh, Soumitra S.
6  TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE
7  TITLE OF INVENTION: TRANSLOCATOR (ANT), NOVEL ANT LIGANDS AND SCREENING ASSAYS
8  TITLE OF INVENTION: THEREFOR
9  FILE REFERENCE: 660088.420
10 CURRENT APPLICATION NUMBER: US/09/185,904A
11 CURRENT FILING DATE: 1998-11-03
12 NUMBER OF SEQ ID NOS: 33
13 SOFTWARE: FastSeq for Windows Version 3.0
14 SEQ ID NO 31
15 LENGTH: 297
16 TYPE: PRY
17 ORGANISM: Homo sapien
18 US-09-185-904A-31

```

| | | | | |
|-----------------------|----------------|--|----------|------------|
| Query Match | 100.0% | Score 1553 | DB 10 | Length 297 |
| Best Local Similarity | 100.0% | Pred. No. 1,3e-160 | | |
| Matches 297 | Conservative 0 | Mismatches 0 | Indels 0 | Gaps 0 |
| QY | 1 | MGDHAMSLKDLDTLGAVALAAVSKTAVALTEEVKLLLOVQAHSAKQISAEKQYKGIIDCYVR | 60 | |
| Db | 1 | MGDHAMSLKDLDTLGAVALAAVSKTAVALTEEVKLLLOVQAHSAKQISAEKQYKGIIDCYVR | 60 | |
| QY | 61 | IPKEQGFSEFWRGNLANVIRYFPPQALFARFKDYKQKFLGVDYDHKQFWMYFAGNLSAG | 120 | |
| Db | 61 | IPKEQGFSEFWRGNLANVIRYFPPQALFARFKDKYKQFLGVDYDHKQFWMYFAGNLSAG | 120 | |
| QY | 121 | GAAGATSLCEFYPLDFAFRTLAADYGRRAQEEFHGLGDCIIRKSDGLRGLYQGFENVSY | 180 | |
| Db | 121 | GAAGATSLCEFYPLDFAFRTLAADYGRRAQEEFHGLGDCIIRKSDGLRGLYQGFENVSY | 180 | |
| QY | 181 | QGIITTYRAAYFGVYDTAKGMLPDERNVHIEFSWMAIOSVTAAGLSYFEDTVRRMMQ | 240 | |
| Db | 181 | QGIITTYRAAYFGVYDTAKGMLPDERNVHIEFSWMAIOSVTAAGLSYFEDTVRRMMQ | 240 | |
| QY | 241 | SGRRGADIMTYGVDCKRRTAKDKDGAARFEGGANSVNRGNGGAFVLYLYDEIKKYY | 297 | |
| Db | 241 | SGRRGADIMTYGVDCKRRTAKDKDGAARFEGGANSVNRGNGGAFVLYLYDEIKKYY | 297 | |

RESULT 4
 US-09-811-094-32
 : Sequence 32, Application US/09811094
 : Patient No. US20010044144A1
 : GENERAL INFORMATION:
 : APPLICANT: Anderson, Christen M.
 : APPLICANT: Davis, Robert E.
 : APPLICANT: Clevenger, William
 : APPLICANT: Willey, Sandra Eileen
 : APPLICANT: Miller, Scott W.
 : APPLICANT: Scabo, Tomas R.
 : APPLICANT: Ghosh, Soumitra S.
 : APPLICANT: Moos, Walter H.
 : APPLICANT: Pei, Yezhong
 : TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLATOR (ANT),
 : TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR
 : FILE REFERENCE: 660088.42004
 : CURRENT APPLICATION NUMBER: US/09/811,094
 : CURRENT FILING DATE: 2001-03-14
 : NUMBER OF SEQ. ID NOS: 37
 : SOFTWARE: FastSeq for Windows Version 3.0

| | | |
|-----------------------|--------|---------------------------------|
| US-09-811-094-32 | ; | ORGANISM: Homo sapien |
| Query Match | 89.6%; | Score 1391.5; DB 9; Length 298; |
| Best Local Similarity | 88.6%; | Pred. No. 5e-143; |

Matches 263; Conservative 17; Mismatches 16; Indels 1; Gaps 1;

QY 1 MGDHMSFLKDFLAGAANAASKTAVAPIERVKLLLOVHASKOISAEKQKGIIDCYVR 60
 DB 1 MTDAAISFAKDFLAGVAANAISKTAVAPIERVKLLLOVHASKOITADKQKGIIDCYVR 60
 QY 61 IPKQEGFLSFWRGNLANVIRFPFOALNFAFKDKYKQFLGVDNRHKOFRWRFAGNLSG 120
 DB 61 IPKQEVLSFWRGNLANVIRFPFOALNFAFKDKYKQFLGVDNRHKOFRWRFAGNLSG 120
 QY 121 GAAGATSLCFYPPDFAFTRIAADVGR-AOREFHGIDDCIIRKISGSLGKLYOGFNVS 179
 DB 121 GAAGATSLCFYPPDFAFTRIAADVGR-AOREFHGIDDCIIRKISGSLGKLYOGFNVS 180
 QY 180 VOGIIIRAAAFGYIDTAAGKMLPDPKNVHIFVSMIAOSYAVAGLSTYPEDTVRRMM 239
 DB 181 VOGIIIRAAAFGYIDTAAGKMLPDPKNVHIFVSMIAOSYAVAGLSTYPEDTVRRMM 240
 QY 240 QSGRKGADIMYTGTLDCWRKTIARDEGKAFKFGAMSNVLRGMAFVLVLYDEIKKY 296
 DB 241 QSGRKGADIMYTGTLDCWRKTIARDEGKAFKFGAMSNVLRGMAFVLVLYDEIKKY 297

RESULT 5

US-09-810-644-32
 ; Sequence 32, Application US/09810644
 ; Patent No. US20020012992A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Anderson, Christen M.
 ; APPLICANT: Davis, Robert E.
 ; APPLICANT: Clevenger, William
 ; APPLICANT: Wiley, Sandra Eileen
 ; APPLICANT: Miller, Scott W.
 ; APPLICANT: Szabo, Tomas R.
 ; APPLICANT: Ghosh, Soumitra S.
 ; APPLICANT: Moos, Walter H.
 ; TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),
 ; FILE REFERENCE: 660088.420D3
 ; CURRENT APPLICATION NUMBER: US/09/810,644
 ; CURRENT FILING DATE: 2001-03-14
 ; NUMBER OF SEQ ID NOS: 37
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 32
 ; LENGTH: 298
 ; TYPE: PRT
 ; ORGANISM: Homo sapien
 US-09-810-644-32

Query Match 89.6%; Score 1391.5; DB 9; Length 298;
 Best Local Similarity 88.6%; Pred. No. 5e-143;
 Matches 263; Conservative 17; Mismatches 16; Indels 1; Gaps 1;

QY 1 MGDHMSFLKDFLAGAANAASKTAVAPIERVKLLLOVHASKOISAEKQKGIIDCYVR 60
 DB 1 MTDAAISFAKDFLAGVAANAISKTAVAPIERVKLLLOVHASKOITADKQKGIIDCYVR 60
 QY 61 IPKQEGFLSFWRGNLANVIRFPFOALNFAFKDKYKQFLGVDNRHKOFRWRFAGNLSG 120
 DB 61 IPKQEVLSFWRGNLANVIRFPFOALNFAFKDKYKQFLGVDNRHKOFRWRFAGNLSG 120
 QY 121 GAAGATSLCFYPPDFAFTRIAADVGR-AOREFHGIDDCIIRKISGSLGKLYOGFNVS 179
 DB 121 GAAGATSLCFYPPDFAFTRIAADVGR-AOREFHGIDDCIIRKISGSLGKLYOGFNVS 180
 QY 180 VOGIIIRAAAFGYIDTAAGKMLPDPKNVHIFVSMIAOSYAVAGLSTYPEDTVRRMM 239
 DB 181 VOGIIIRAAAFGYIDTAAGKMLPDPKNVHIFVSMIAOSYAVAGLSTYPEDTVRRMM 240
 QY 240 QSGRKGADIMYTGTLDCWRKTIARDEGKAFKFGAMSNVLRGMAFVLVLYDEIKKY 296
 DB 241 QSGRKGADIMYTGTLDCWRKTIARDEGKAFKFGAMSNVLRGMAFVLVLYDEIKKY 297

RESULT 6

US-09-185-904A-32
 ; Sequence 32, Application US/09185904A
 ; Patent No. US20020177185A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Anderson, Christen M.
 ; APPLICANT: Davis, Robert E.
 ; APPLICANT: Clevenger, William
 ; APPLICANT: Wiley, Sandra Eileen
 ; APPLICANT: Miller, Scott W.
 ; APPLICANT: Szabo, Tomas R.
 ; APPLICANT: Ghosh, Soumitra S.
 ; TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE
 ; FILE REFERENCE: 660088.420
 ; CURRENT APPLICATION NUMBER: US/09/185,904A
 ; CURRENT FILING DATE: 1998-11-03
 ; NUMBER OF SEQ ID NOS: 33
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 32
 ; LENGTH: 298
 ; TYPE: PRT
 ; ORGANISM: Homo sapien
 US-09-185-904A-32

Query Match 89.6%; Score 1391.5; DB 10; Length 298;
 Best Local Similarity 88.6%; Pred. No. 5e-143;
 Matches 263; Conservative 17; Mismatches 16; Indels 1; Gaps 1;

QY 1 MGDHMSFLKDFLAGAANAASKTAVAPIERVKLLLOVHASKOISAEKQKGIIDCYVR 60
 DB 1 MTDAAISFAKDFLAGVAANAISKTAVAPIERVKLLLOVHASKOITADKQKGIIDCYVR 60
 QY 61 IPKQEGFLSFWRGNLANVIRFPFOALNFAFKDKYKQFLGVDNRHKOFRWRFAGNLSG 120
 DB 61 IPKQEVLSFWRGNLANVIRFPFOALNFAFKDKYKQFLGVDNRHKOFRWRFAGNLSG 120
 QY 121 GAAGATSLCFYPPDFAFTRIAADVGR-AOREFHGIDDCIIRKISGSLGKLYOGFNVS 179
 DB 121 GAAGATSLCFYPPDFAFTRIAADVGR-AOREFHGIDDCIIRKISGSLGKLYOGFNVS 180
 QY 180 VOGIIIRAAAFGYIDTAAGKMLPDPKNVHIFVSMIAOSYAVAGLSTYPEDTVRRMM 239
 DB 181 VOGIIIRAAAFGYIDTAAGKMLPDPKNVHIFVSMIAOSYAVAGLSTYPEDTVRRMM 240
 QY 240 QSGRKGADIMYTGTLDCWRKTIARDEGKAFKFGAMSNVLRGMAFVLVLYDEIKKY 296
 DB 241 QSGRKGADIMYTGTLDCWRKTIARDEGKAFKFGAMSNVLRGMAFVLVLYDEIKKY 297

RESULT 7

US-09-811-094-33
 ; Sequence 33, Application US/09811094
 ; Patent No. US20010044144A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Anderson, Christen M.
 ; APPLICANT: Davis, Robert E.
 ; APPLICANT: Clevenger, William
 ; APPLICANT: Wiley, Sandra Eileen
 ; APPLICANT: Miller, Scott W.
 ; APPLICANT: Szabo, Tomas R.
 ; APPLICANT: Ghosh, Soumitra S.
 ; APPLICANT: Moos, Walter H.
 ; TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),
 ; FILE REFERENCE: 660088.420D4
 ; CURRENT APPLICATION NUMBER: US/09/811,094
 ; CURRENT FILING DATE: 2001-03-14
 ; NUMBER OF SEQ ID NOS: 37

GenCore version 5.1.6
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OW protein - protein search, using sw model

Run on: August 28, 2003, 19:35:01 ; Search time 20.6204 Seconds

(without alignments)
1385.139 Million cell updates/sec

Title: US-09-811-132-31

Perfect score: 1553

Sequence: 1 MGDHMSFLKDFLAGAVALA.....LRGNGAFVLVDEIKKYV 297

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : PIR_76:*

1: pir1:*

2: pir2:*

3: pir3:*

4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match Length | DB ID | Description |
|------------|--------|--------------------|-------|--------------------|
| 1 | 1526.5 | 98.3 | 298 1 | ADP,ATP carrier pr |
| 2 | 1466.5 | 94.4 | 298 2 | adenine nucleotide |
| 3 | 1463.5 | 94.2 | 298 2 | ADP,ATP carrier pr |
| 4 | 1458.5 | 93.9 | 298 1 | ADP,ATP carrier pr |
| 5 | 1391.5 | 89.6 | 298 1 | ADP,ATP carrier pr |
| 6 | 1385.5 | 89.2 | 298 1 | ADP,ATP carrier pr |
| 7 | 1380.5 | 88.9 | 298 2 | ADP,ATP carrier pr |
| 8 | 1368.5 | 88.1 | 298 2 | ADP,ATP carrier pr |
| 9 | 1142.5 | 73.6 | 301 1 | ADP,ATP carrier pr |
| 10 | 1045.5 | 67.3 | 313 2 | ADP,ATP carrier pr |
| 11 | 1043.5 | 67.2 | 313 2 | ADP,ATP carrier pr |
| 12 | 1037.5 | 66.8 | 300 2 | ADP,ATP carrier pr |
| 13 | 1005.5 | 64.7 | 300 2 | ADP,ATP carrier pr |
| 14 | 973.5 | 62.7 | 339 2 | ADP,ATP carrier pr |
| 15 | 904.5 | 58.2 | 301 2 | ADP,ATP carrier pr |
| 16 | 772 | 49.7 | 306 1 | ADP,ATP carrier pr |
| 17 | 770.5 | 49.6 | 306 1 | ADP,ATP carrier pr |
| 18 | 756.5 | 48.7 | 387 2 | ADP,ATP carrier pr |
| 19 | 752.5 | 48.5 | 322 2 | ADP,ATP carrier pr |
| 20 | 752.5 | 48.5 | 322 2 | ADP,ATP carrier pr |
| 21 | 751.5 | 48.4 | 387 2 | ADP,ATP carrier pr |
| 22 | 746.5 | 48.1 | 379 2 | ADP,ATP carrier pr |
| 23 | 746.5 | 48.1 | 382 2 | ADP,ATP carrier pr |
| 24 | 745.5 | 48.0 | 326 2 | ADP,ATP carrier pr |
| 25 | 745.5 | 48.0 | 386 2 | ADP,ATP carrier pr |
| 26 | 744.5 | 47.9 | 386 2 | ADP,ATP carrier pr |
| 27 | 740 | 47.6 | 379 2 | ADP,ATP carrier pr |
| 28 | 740 | 47.6 | 386 2 | ADP,ATP carrier pr |
| 29 | 737 | 47.5 | 385 1 | ADP,ATP carrier pr |

| | | | | |
|----|-------|------|-------|--------------------|
| 30 | 736 | 47.4 | 307 2 | ADP,ATP carrier pr |
| 31 | 734 | 47.3 | 318 1 | ADP,ATP carrier pr |
| 32 | 733.5 | 47.2 | 313 1 | ADP,ATP carrier pr |
| 33 | 729 | 46.9 | 305 2 | ADP,ATP carrier pr |
| 34 | 728.5 | 46.9 | 306 2 | ADP,ATP carrier pr |
| 35 | 718.5 | 46.3 | 309 2 | ADP,ATP carrier pr |
| 36 | 676 | 43.5 | 298 2 | ADP,ATP carrier pr |
| 37 | 508 | 32.7 | 327 2 | ADP,ATP carrier pr |
| 38 | 368 | 23.7 | 415 2 | ADP,ATP carrier pr |
| 39 | 367.5 | 23.7 | 415 2 | ADP,ATP carrier pr |
| 40 | 363 | 23.4 | 381 2 | ADP,ATP carrier pr |
| 41 | 350.5 | 22.6 | 475 2 | ADP,ATP carrier pr |
| 42 | 349.5 | 22.5 | 352 2 | ADP,ATP carrier pr |
| 43 | 345.5 | 22.2 | 358 2 | ADP,ATP carrier pr |
| 44 | 334.5 | 21.5 | 348 2 | ADP,ATP carrier pr |
| 45 | 327 | 21.1 | 332 2 | ADP,ATP carrier pr |

ALIGNMENTS

RESULT 1
AA4778
ADP,ATP carrier protein T1 - human
N:Alternate names: mitochondrial ADP,ATP translocase 1
C:Species: Homo sapiens (man)
C:Date: 17-Mar-2000 #sequence,revision 17-Mar-2000 #text_change 17-Mar-2000
C:Accession: AA4778; S03893; A39891; A28116
R:Li, K.; Warner, C.K.; Hodges, J.A.; Minoshima, S.; Kudoh, J.; Fukuyama, R.; Maekawa, J. Biol. Chem. 264, 13998-14004, 1989
A:Title: A human muscle adenine nucleotide translocator gene has four exons, is located
A:Reference number: AA4778; MUID:89340499; PMID:2547778
A:Accession: AA4778
A:Status: preliminary
A:Molecule type: DNA
A:Residues: 1-298 <LIA>
A:Cross-references: GB:J04982; NID:9178658; PIDN:AAA51736.1; PID:9178659
R:Cozens, A.L.; Runswick, M.J.; Walker, J.E.
J. Mol. Biol. 206, 261-280, 1989
A:Title: DNA sequences of two expressed nuclear genes for human mitochondrial ADP/ATP
A:Reference number: S03893; MUID:89336596; PMID:2541251
A:Accession: S03893
A:Status: not compared with conceptual translation
A:Molecule type: DNA
A:Residues: 1-298 <COZ>
R:Neckelmann, N.; Li, K.; Wade, R.P.; Shuster, R.; Wallace, D.C.
Proc. Natl. Acad. Sci. U.S.A. 84, 7580-7584, 1987
A:Title: cDNA sequence of a human skeletal muscle ADP/ATP translocator: lack of a lea
A:Reference number: A39891; MUID:88041149; PMID:2823266
A:Accession: A39891
A:Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-15, 'A', 17-146, 'RR', 149, 151-226, 'L', 228-298 <NEC>
A:Cross-references: GB:J02966; NID:9339919; PIDN:AAA61223.1; PID:9339920
A:Experimental source: clone PHMAN7
R:Houldsworth, J.; Attardi, G.
Proc. Natl. Acad. Sci. U.S.A. 85, 377-381, 1988
A:Title: Two distinct genes for ADP/ATP translocase are expressed at the mRNA level 1
A:Reference number: A94197; MUID:86124645; PMID:2829183
A:Accession: A28116
A:Molecule type: mRNA
A:Residues: 1-37 <HOU>
A:Cross-references: GB:J03593; NID:9339724; PIDN:AAA36751.1; PID:9339725
A:Experimental source: liver
A:Genetics:
A:Gene: GDB:AMT1; T1
A:Cross-references: GDB:119680; OMIM:103220
A:Map position: 4q35-4q35
C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology
C:Keywords: duplication; homodimer; mitochondrial; transmembrane protein
F:2-298/Product: ADP,ATP carrier protein #status predicted <MAT>
F:5-99/Domain: ADP,ATP carrier protein repeat homology <ACP1>
F:110-202/Domain: ADP,ATP carrier protein repeat homology <ACP2>

F:207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>

Query Match 98.3%; Score 1526.5; DB 1; Length 298;
Best Local Similarity 98.3%; Pred. No. 1.5e-130;
Matches 293; Conservative 2; Mismatches 2; Indels 1; Gaps 1;

QY 1 MGDHMSFLKDFLAGVAAVSTKTAAPIERVKLLQVQHASQKISAEKQYKGIIDCVNR 60
|||||
DB 1 MGDHMSFLKDFLAGVAAVSTKTAAPIERVKLLQVQHASQKISAEKQYKGIIDCVNR 60
QY 61 IPKEQGLSFWRKGNLANVIRYPTQALNFAFKDKYKQIFGVDNRHKKQFRYFAGNLAG 120
|||||
DB 61 IPKEQGLSFWRKGNLANVIRYPTQALNFAFKDKYKQIFGVDNRHKKQFRYFAGNLAG 120
QY 121 GAAGATSLCFVYPLDFARTRLADVGR-RAQREFHGLGDCIIRKFSKDGRLGLYQGFNVS 179
|||||
DB 121 GAAGATSLCFVYPLDFARTRLADVGR-RAQREFHGLGDCIIRKFSKDGRLGLYQGFNVS 180
QY 180 VQGIITIRAAVFEVYDTAKGMLDPKKNVHIFVSMIAQSVTAAGLSTYFPDVRRRMM 239
|||||
DB 181 VQGIITIRAAVFEVYDTAKGMLDPKKNVHIFVSMIAQSVTAAGLSTYFPDVRRRMM 240
QY 240 QSGRKADIMYTGTVDCMRKIARDEGAKAFKGAWSNVLRGMGAFVLYLDEIKRYV 297
|||||
DB 241 QSGRKADIMYTGTVDCMRKIARDEGAKAFKGAWSNVLRGMGAFVLYLDEIKRYV 298

RESULT 2

160173

adenine nucleotide translocator - rat

C:Species: Rattus norvegicus (Norway rat)

C>Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 20-Aug-1999

C:Accession: 160173

R:Shinohara, Y.; Kamida, M.; Yamazaki, N.; Terada, H.

Biochim. Biophys. Acta 1152, 192-196, 1993

A:Title: Isolation and characterization of cDNA clones and a genomic clone encoding rat

A:Reference number: 160173; MUID:94002161; PMID:8399300

A:Accession: 160173

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-298 <RES>

A:Cross-references: EMBL:X61667; NID:9400426; PIDN:CAA3842.1; PID:9400427

C:Genetics:

A:Gene: anti

A:Insertions: 37/3; 200/1; 247/1

C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology

C:Keywords: duplication; transmembrane protein

F:5-99/Domain: ADP,ATP carrier protein repeat homology <ACP1>

F:110-202/Domain: ADP,ATP carrier protein repeat homology <ACP2>

F:207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>

Query Match 94.4%; Score 1466.5; DB 2; Length 298;

Best Local Similarity 94.3%; Pred. No. 4.1e-125;

Matches 281; Conservative 9; Mismatches 7; Indels 1; Gaps 1;

QY 1 MGDHMSFLKDFLAGVAAVSTKTAAPIERVKLLQVQHASQKISAEKQYKGIIDCVNR 60
|||||
DB 1 MGDHMSFLKDFLAGVAAVSTKTAAPIERVKLLQVQHASQKISAEKQYKGIIDCVNR 60
QY 61 IPKEQGLSFWRKGNLANVIRYPTQALNFAFKDKYKQIFGVDNRHKKQFRYFAGNLAG 120
|||||
DB 61 IPKEQGLSFWRKGNLANVIRYPTQALNFAFKDKYKQIFGVDNRHKKQFRYFAGNLAG 120
QY 121 GAAGATSLCFVYPLDFARTRLADVGR-RAQREFHGLGDCIIRKFSKDGRLGLYQGFNVS 179
|||||
DB 121 GAAGATSLCFVYPLDFARTRLADVGR-RAQREFHGLGDCIIRKFSKDGRLGLYQGFNVS 180
QY 180 VQGIITIRAAVFEVYDTAKGMLDPKKNVHIFVSMIAQSVTAAGLSTYFPDVRRRMM 239
|||||
DB 181 VQGIITIRAAVFEVYDTAKGMLDPKKNVHIFVSMIAQSVTAAGLSTYFPDVRRRMM 240
QY 240 QSGRKADIMYTGTVDCMRKIARDEGAKAFKGAWSNVLRGMGAFVLYLDEIKRYV 297
|||||

DB 241 QSGRKADIMYTGTVDCMRKIARDEGAKAFKGAWSNVLRGMGAFVLYLDEIKRYV 298

RESULT 3

S37210

ADP,ATP carrier protein T1 - mouse

N:Alternate names: adenine nucleotide carrier

C:Species: Mus musculus (house mouse)

C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Aug-1999

C:Accession: S37210

R:Laplace, C.; Costet, P.

submitted to the EMBL Data Library, September 1993

A:Reference number: S37210

A:Accession: S37210

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-298 <IAP>

A:Cross-references: EMBL:X74510; NID:9402627; PIDN:CAA52616.1; PID:9402628

C:Genetics:

A:Gene: ANCI

C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology

F:5-99/Domain: ADP,ATP carrier protein repeat homology <ACP1>

F:110-202/Domain: ADP,ATP carrier protein repeat homology <ACP2>

F:207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>

Query Match 94.2%; Score 1463.5; DB 2; Length 298;

Best Local Similarity 94.0%; Pred. No. 7.6e-125;

Matches 280; Conservative 10; Mismatches 7; Indels 1; Gaps 1;

QY 1 MGDHMSFLKDFLAGVAAVSTKTAAPIERVKLLQVQHASQKISAEKQYKGIIDCVNR 60
|||||
DB 1 MGDHMSFLKDFLAGVAAVSTKTAAPIERVKLLQVQHASQKISAEKQYKGIIDCVNR 60
QY 61 IPKEQGLSFWRKGNLANVIRYPTQALNFAFKDKYKQIFGVDNRHKKQFRYFAGNLAG 120
|||||
DB 61 IPKEQGLSFWRKGNLANVIRYPTQALNFAFKDKYKQIFGVDNRHKKQFRYFAGNLAG 120
QY 121 GAAGATSLCFVYPLDFARTRLADVGR-RAQREFHGLGDCIIRKFSKDGRLGLYQGFNVS 179
|||||
DB 121 GAAGATSLCFVYPLDFARTRLADVGR-RAQREFHGLGDCIIRKFSKDGRLGLYQGFNVS 180
QY 180 VQGIITIRAAVFEVYDTAKGMLDPKKNVHIFVSMIAQSVTAAGLSTYFPDVRRRMM 239
|||||
DB 181 VQGIITIRAAVFEVYDTAKGMLDPKKNVHIFVSMIAQSVTAAGLSTYFPDVRRRMM 240
QY 240 QSGRKADIMYTGTVDCMRKIARDEGAKAFKGAWSNVLRGMGAFVLYLDEIKRYV 297
|||||
DB 241 QSGRKADIMYTGTVDCMRKIARDEGAKAFKGAWSNVLRGMGAFVLYLDEIKRYV 298

RESULT 4

XMB0

ADP,ATP carrier protein T1 - bovine

N:Alternate names: ADP/ATP translocase T1

C:Species: Bos primigenius taurus (cattle)

C>Date: 14-Nov-1983 #sequence_revision 22-Jul-1994 #text_change 22-Jun-1999

C:Accession: A43646; A24822; A03181; A61343; S69369

R:Powell, S.J.; Medd, S.M.; Runswick, M.J.; Walker, J.E.

Biochemistry 28, 866-873, 1989

A:Title: Two bovine genes for mitochondrial ADP/ATP translocase expressed differently

A:Reference number: A43646; MUID:89229093; PMID:2540808

A:Accession: A43646

A:Molecule type: mRNA

A:Residues: 1-298 <POW>

A:Cross-references: GB:M24102; NID:9529414; PIDN:AAA30768.1; PID:9529415

R:Rasmussen, U.B.; Wohlrab, H.

Biochem. Biophys. Res. Commun. 138, 850-857, 1986

A:Title: Bovine cardiac mitochondrial ADP/ATP-carrier: two distinct mRNAs and an unus

A:Reference number: A24822; MUID:86295775; PMID:3017341

A:Accession: A24822

A:Molecule type: mRNA

A:Residues: 208-298 <RAS>

A:Cross-references: GB:M13783; NID:g162630; PIDN:AAA30363.1; PID:g162631
 R:Aquila, H.; Mistra, D.; Eulitz, M.; Klingenberg, M.
 Hoppe-Seyler's Z. Physiol. Chem. 363, 345-349, 1982
 A:Title: Complete amino acid sequence of the ADP/ATP carrier from beef heart mitochondrion
 A:Reference number: A03181; MUID:82188267; PMID:7076130
 A:Accession: A03181
 A:Molecule type: protein
 A:Residues: 2-51, 'X', '53-70', 'X', '72-109', 'X', '111-298' <A0U>
 A:Note: residue 52 may be methyllysine
 R:Babel, M.; Machter, E.; Aquila, H.; Klingenberg, M.
 Biochim. Biophys. Acta 670, 176-180, 1981
 A:Title: Amino acid sequence determination of the ADP/ATP carrier from beef heart mitochondrion
 A:Reference number: A61343; MUID:82046808; PMID:6271240
 A:Accession: A61343
 A:Molecule type: protein
 A:Residues: 205-298 <BAB>
 R:Oetmeier, W.; Masson, K.; Kalina, S.
 Eur. J. Biochem. 227, 730-733, 1995
 A:Title: ((3)H)-2,4-dichloro-5-isopropylisocitrate labels Cys159 of the bovine mitochondrial ADP/ATP carrier
 A:Reference number: S69369; MUID:95172058; PMID:7867632
 A:Accession: S69369
 A:Molecule type: protein
 A:Residues: 49-63;154-168 <OET>
 C:Comment: This protein is synthesized in the cytosol and transported into the mitochondrion
 C:Complex: homodimer
 C:Function:
 A:Description: catalyzes the exchange between cytosolic ADP and mitochondrial ATP
 A:Note: located in the inner mitochondrial membrane
 C:Superfamily: ADP/ATP carrier protein; ADP/ATP carrier protein repeat homology
 C:Keywords: acetylated amino end; duplication; homodimer; methylated amino acid; mtocch
 F:5-99/Domain: ADP/ATP carrier protein repeat homology <ACP1>
 F:110-202/Domain: ADP/ATP carrier protein repeat homology <ACP2>
 F:207-298/Domain: ADP/ATP carrier protein repeat homology <ACP3>
 F:2/Modified site: acetylated amino end (Ser) (in mature form) #status experimental
 F:52/Modified site: N6-methyllysine (Lys) #status predicted

Query Match 93.9%; Score 1458.5; DB 1; Length 298;
 Best Local Similarity 94.3%; Pred. No. 2.2e-124;
 Matches 281; Conservative 7; Mismatches 9; Indels 1; Gaps 1;

QY 1 MGDHMSFLKDFLAGVAAVAAVSKTAVAPTERKLLQVHASKQISAEKQYGIIDCYVR 60
 DB 1 MSDALSLKDFLAGVAAVAAVSKTAVAPTERKLLQVHASKQISAEKQYGIIDCYVR 60
 QY 61 IPKEGFLSFMKGNLANVIRYPTQALNFAFKDKYKQFLGVDNRHKKQFWRFFAGNLSG 120
 DB 61 IPKEGFLSFMKGNLANVIRYPTQALNFAFKDKYKQFLGVDNRHKKQFWRFFAGNLSG 120
 QY 121 GAAGTSLCFYVPLDFARTRLAADYGR-RAQREFHGLDCTIKIRKSDGLRGLYGFNVS 179
 DB 121 GAAGTSLCFYVPLDFARTRLAADYGR-RAQREFHGLDCTIKIRKSDGLRGLYGFNVS 179
 QY 180 VOGIIIRAAVFGVDTAKGMLDPRKNVHIFVSMIAQSVTVAGLSVPEPTVRRMM 239
 DB 180 VOGIIIRAAVFGVDTAKGMLDPRKNVHIFVSMIAQSVTVAGLSVPEPTVRRMM 239
 QY 240 QSGRKADIMYGTGTCWKRIKADGAKAFKFGANSNVLKRGCAFVLVLYDEIKKY 297
 DB 240 QSGRKADIMYGTGTCWKRIKADGAKAFKFGANSNVLKRGCAFVLVLYDEIKKY 297
 A:Title: Molecular cloning of a cDNA for a human ADP/ATP carrier which is growth-regulated
 A:Reference number: A29132; MUID:87166056; PMID:3031073
 A:Accession: A29132

RESULT 5
 A29132
 ADP/ATP carrier protein T2 - human
 N:Alternate names: mitochondrial ADP/ATP translocase 2
 C:Species: Homo sapiens (man)
 C:Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 17-Mar-2000
 C:Accession: A29132; C28116
 R:Battini, R.; Ferrari, S.; Kaczmarek, L.; Calabretta, B.; Chen, S.; Baserga, R.
 J. Biol. Chem. 262, 4355-4359, 1987
 A:Title: Molecular cloning of a cDNA for a human ADP/ATP carrier which is growth-regulated
 A:Reference number: A29132; MUID:87166056; PMID:3031073
 A:Accession: A29132

A:Molecule type: mRNA
 A:Residues: 1-298 <BAT>
 A:Cross-references: GB:J02683; NID:g179246; PIDN:AAA35579.1; PID:g179247
 R:Houldsworth, J.; Attardi, G.
 Proc. Natl. Acad. Sci. U.S.A. 85, 377-381, 1988
 A:Title: Two distinct genes for ADP/ATP translocase are expressed at the mRNA level 1
 A:Reference number: A94197; MUID:88124845; PMID:2829183
 A:Accession: C28116
 A:Molecule type: mRNA
 A:Residues: 47-65, 'G', '67-110', 'L', '112-161', 'G', '163-298' <HOU>
 A:Cross-references: GB:J03591; NID:g339720; PIDN:AAA36749.1; PID:g339721
 A:Experimental source: clone PHAT3
 C:Genetics:
 A:Gene: GDB:AMT2; T3; 2F1
 A:Cross-references: GDB:125190; OMIM:300150
 A:Map position: Xq13-qx26
 A:Note: there may be some confusion in the assignment of sequences for GDB:AMT2 and G
 C:Superfamily: ADP/ATP carrier protein; ADP/ATP carrier protein repeat homology
 C:Keywords: duplication; homodimer; mitochondrion; transmembrane protein
 F:5-99/Domain: ADP/ATP carrier protein repeat homology <ACP1>
 F:110-202/Domain: ADP/ATP carrier protein repeat homology <ACP2>
 F:207-298/Domain: ADP/ATP carrier protein repeat homology <ACP3>

Query Match 89.6%; Score 1391.5; DB 1; Length 298;
 Best Local Similarity 88.6%; Pred. No. 2.5e-118;
 Matches 263; Conservative 17; Mismatches 16; Indels 1; Gaps 1;

QY 1 MGDHMSFLKDFLAGVAAVAAVSKTAVAPTERKLLQVHASKQISAEKQYGIIDCYVR 60
 DB 1 MGDALSLKDFLAGVAAVAAVSKTAVAPTERKLLQVHASKQITADQYGIIDCYVR 60
 QY 61 IPKEGFLSFMKGNLANVIRYPTQALNFAFKDKYKQFLGVDNRHKKQFWRFFAGNLSG 120
 DB 61 IPKEGFLSFMKGNLANVIRYPTQALNFAFKDKYKQFLGVDNRHKKQFWRFFAGNLSG 120
 QY 121 GAAGTSLCFYVPLDFARTRLAADYGR-RAQREFHGLDCTIKIRKSDGLRGLYGFNVS 179
 DB 121 GAAGTSLCFYVPLDFARTRLAADYGR-RAQREFHGLDCTIKIRKSDGLRGLYGFNVS 179
 QY 180 VOGIIIRAAVFGVDTAKGMLDPRKNVHIFVSMIAQSVTVAGLSVPEPTVRRMM 239
 DB 180 VOGIIIRAAVFGVDTAKGMLDPRKNVHIFVSMIAQSVTVAGLSVPEPTVRRMM 239
 QY 240 QSGRKADIMYGTGTCWKRIKADGAKAFKFGANSNVLKRGCAFVLVLYDEIKKY 296
 DB 240 QSGRKADIMYGTGTCWKRIKADGAKAFKFGANSNVLKRGCAFVLVLYDEIKKY 296
 A:Title: DNA sequences of two expressed nuclear genes for human mitochondrial ADP/ATP
 A:Reference number: S03893; MUID:89336396; PMID:2541251
 A:Accession: S03894
 A:Status: not compared with conceptual translation
 A:Molecule type: DNA
 A:Residues: 1-298 <COZ>
 R:Houldsworth, J.; Attardi, G.
 Proc. Natl. Acad. Sci. U.S.A. 85, 377-381, 1988
 A:Title: Two distinct genes for ADP/ATP translocase are expressed at the mRNA level 1
 A:Reference number: A94197; MUID:88124845; PMID:2829183
 A:Accession: B28116
 A:Molecule type: mRNA
 A:Residues: 36-104, 'R', '106', 'A', '109-298' <HOU>
 A:Cross-references: GB:J03592; NID:g339722; PIDN:AAA36750.1; PID:g339723
 A:Experimental source: liver
 C:Genetics:

RESULT 6
 S03894
 ADP/ATP carrier protein T3 - human
 N:Alternate names: ADP/ATP carrier protein T2 (misidentification); mitochondrial ADP/
 C:Species: Homo sapiens (man)
 C:Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 17-Mar-2000
 C:Accession: S03894; B28116
 R:Cozens, A.L.; Runswick, M.J.; Walker, J.E.
 J. Mol. Biol. 206, 261-280, 1989
 A:Title: DNA sequences of two expressed nuclear genes for human mitochondrial ADP/ATP
 A:Reference number: S03893; MUID:89336396; PMID:2541251
 A:Accession: S03894
 A:Status: not compared with conceptual translation
 A:Molecule type: DNA
 A:Residues: 1-298 <COZ>
 R:Houldsworth, J.; Attardi, G.
 Proc. Natl. Acad. Sci. U.S.A. 85, 377-381, 1988
 A:Title: Two distinct genes for ADP/ATP translocase are expressed at the mRNA level 1
 A:Reference number: A94197; MUID:88124845; PMID:2829183
 A:Accession: B28116
 A:Molecule type: mRNA
 A:Residues: 36-104, 'R', '106', 'A', '109-298' <HOU>
 A:Cross-references: GB:J03592; NID:g339722; PIDN:AAA36750.1; PID:g339723
 A:Experimental source: liver
 C:Genetics:

F:112-204/Domain: ADP,ATP carrier protein repeat homology <ACFP2>
F:209-300/Domain: ADP,ATP carrier protein repeat homology <ACFP3>

Query Match 73.6%; Score 1142.5; DB 1; Length 301;
Best Local Similarity 76.2%; Pred. No. 8.8e-96;
Matches 221; Conservative 26; Mismatches 42; Indels 1; Gaps 1;

OY 6 WSLFKDLFAGAVAAVSKTAVAPIERVKLLQVOHASKQISAEKQYGIIDCVIRPEKG 65
DB 8 YGFADFLAGGISAAVSKTAVAPIERVKLLQVOHASKQISAEKQYGIIDCVIRPEKG 67
OY 66 GLSFWRGNLANVIRYPTQALNFAFKDKYKQLFLGVDRHKQFRYRAGNLASGGAAGA 125
DB 68 GIGAFEGGNLANVIRYPTQALNFAFKDKYKQVGVDRKQFRYRAGNLASGGAAGA 127
OY 126 TSLFVYPLDFARTRLAADVGRRA-QREFHGIDCIIIFKSDGLRGYGFNVSVQGI 184
DB 128 TSLFVYPLDFARTRLAADVGRRA-QREFHGIDCIIIFKSDGLRGYGFNVSVQGI 187
OY 185 IYRAAFEGVDYTAGMLPDPKRVHIFVSMIAQSVTAVAGLSTYPTVRRMMQSGRK 244
DB 188 IYRAAFEGVDYTAGMLPDPKRVHIFVSMIAQSVTAVAGLSTYPTVRRMMQSGRK 247
OY 245 GADIMYGTVCWKRRIADDEGAKAFKGAWSNVLRGMSGAFVLYLYEIKRY 294
DB 248 KSEVMYKNTLDCAVKIINKEGMSAMFKGALSNVFRGTGALVLAIVDEIQKFI 313

RESULT 10

T25850
hypothetical protein T01B11.4 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 11-Jan-2000
C:Accession: T25850
R:Geisels, C.; Stellyes, L.
A:Submitted to the EMBL Data Library, December 1996
A:Description: The sequence of C. elegans cosmid T01B11.
A:Reference number: Z20099
A:Accession: T25850
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-313 <GEI>
A:Cross-references: EMBL:U80931, PIDN:AA838001.1; GSPDB:GN00022; CESP:T01B11.4
A:Experimental source: strain Bristol N2; clone T01B11
C:Genetics:
A:Gene: CESP:T01B11.4
A:Map position: 4
A:Introns: 4/1: 191/2
C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology

Query Match 67.3%; Score 1045.5; DB 2; Length 313;
Best Local Similarity 69.8%; Pred. No. 5.6e-87;
Matches 203; Conservative 36; Mismatches 49; Indels 3; Gaps 2;

OY 8 FLKDFLAGAVAAVSKTAVAPIERVKLLQVOHASKQISAEKQYGIIDCVIRPEKG 67
DB 25 FLIDLASGTAAVSKTAVAPIERVKLLQVOHASKQISAEKQYGIIDCVIRPEKG 84
OY 68 LSFWRGNLANVIRYPTQALNFAFKDKYKQLFLGVDRHKQFRYRAGNLASGGAAGA 127
DB 85 ALMRGNLANVIRYPTQALNFAFKDKYKQLFLGVDRHKQFRYRAGNLASGGAAGA 144
OY 128 LCFVYPLDFARTRLAADVGRRAQREFHGIDCIIIFKSDGLRGYGFNVSVQGI 187
DB 145 LCFVYPLDFARTRLAADVGRRAQREFHGIDCIIIFKSDGLRGYGFNVSVQGI 204
OY 188 AAFEGVDYTAGMLPDPKRVHIFVSMIAQSVTAVAGLSTYPTVRRMMQSGRK 246
DB 205 AAFEGVDYTAGMLPDPKRVHIFVSMIAQSVTAVAGLSTYPTVRRMMQSGRK 262
OY 247 DIMYGTVCWKRRIADDEGAKAFKGAWSNVLRGMSGAFVLYLYEIKRY 297
DB 263 DLYKNTLDCAVKIINKEGMSAMFKGALSNVFRGTGALVLAIVDEIQKFI 313

RESULT 11

T23207
hypothetical protein K01H12.2 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 11-Jan-2000
C:Accession: T23207
R:McMurray, A.
A:Submitted to the EMBL Data Library, December 1995

A:Reference number: Z19707
A:Accession: T23207
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-313 <MI>
A:Cross-references: EMBL:Z68218, PIDN:CAA92472.1; GSPDB:GN00022; CESP:K01H12.2
A:Experimental source: clone K01H12
C:Genetics:
A:Gene: CESP:K01H12.2
A:Map position: 4
A:Introns: 4/1: 191/2
C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology

Query Match 67.2%; Score 1043.5; DB 2; Length 313;
Best Local Similarity 69.4%; Pred. No. 8.5e-87;
Matches 202; Conservative 37; Mismatches 49; Indels 3; Gaps 2;

OY 8 FLKDFLAGAVAAVSKTAVAPIERVKLLQVOHASKQISAEKQYGIIDCVIRPEKG 67
DB 25 FLIDLASGTAAVSKTAVAPIERVKLLQVOHASKQISAEKQYGIIDCVIRPEKG 84
OY 68 LSFWRGNLANVIRYPTQALNFAFKDKYKQLFLGVDRHKQFRYRAGNLASGGAAGA 127
DB 85 ALMRGNLANVIRYPTQALNFAFKDKYKQLFLGVDRHKQFRYRAGNLASGGAAGA 144
OY 128 LCFVYPLDFARTRLAADVGRRAQREFHGIDCIIIFKSDGLRGYGFNVSVQGI 187
DB 145 LCFVYPLDFARTRLAADVGRRAQREFHGIDCIIIFKSDGLRGYGFNVSVQGI 204
OY 188 AAFEGVDYTAGMLPDPKRVHIFVSMIAQSVTAVAGLSTYPTVRRMMQSGRK 246
DB 205 AAFEGVDYTAGMLPDPKRVHIFVSMIAQSVTAVAGLSTYPTVRRMMQSGRK 262
OY 247 DIMYGTVCWKRRIADDEGAKAFKGAWSNVLRGMSGAFVLYLYEIKRY 297
DB 263 DLYKNTLDCAVKIINKEGMSAMFKGALSNVFRGTGALVLAIVDEIQKFI 313

RESULT 12

T25371
hypothetical protein T27E9.1 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans
C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 11-Jan-2000
C:Accession: T25371
R:Lloyd, C.
A:Submitted to the EMBL Data Library, November 1996
A:Reference number: Z20024
A:Accession: T25371
A:Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-300 <MI>
A:Cross-references: EMBL:Z82059, PIDN:CAB04874.1; GSPDB:GN00021; CESP:T27E9.1
A:Experimental source: clone T27E9
C:Genetics:
A:Gene: CESP:T27E9.1
A:Map position: 3
A:Introns: 20/1: 41/3; 115/2
C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology

Query Match 66.8%; Score 1037.5; DB 2; Length 300;
Best Local Similarity 69.1%; Pred. No. 2.8e-86;
Matches 201; Conservative 38; Mismatches 49; Indels 3; Gaps 2;

QY 8 FLKDFLAGAANAASKTAVAPIERVKLLQVOHASKOISAEKQYKGIIDCVIRPKQGF 67
 Db 12 FLIDVLAGSCTAAASKTAVAPIERVKLLQVOHASKOISAEKQYKGIIDCVIRPKQGF 71
 QY 68 LSFWRGNLANVIRFPTQALNFAFKDKYKQLFLGVDVRRHKOFRMYFAGNLAGSGAAGATS 127
 Db 72 AALMRGNLANVIRFPTQALNFAFKDKYKQLFLGVDVRRHKOFRMYFAGNLAGSGAAGATS 131
 QY 128 LCFEYPLDFAFRTLRADVGRRAQREFHGLDCCIIFKFSQDGLKGLYOGFVNSVOGIIIR 187
 Db 132 LCFEYPLDFAFRTLRADVGRRAQREFHGLDCCIIFKFSQDGLKGLYOGFVNSVOGIIIR 191
 QY 188 AAFEGYVDIAKGM-L-PDPKRVHIFVSMIAQSTAVAGLLSYFEDYVRRMMQSGRKA 246
 Db 192 AAFEGMDTAKMVFASDQKLNFEPAAGIAQVTVGSGIISYPMDYVRRMMQSGRKA-- 249
 QY 247 DIWYTGVDQMRKIAKDEGAKAFKGMNSVLRGMSGAFVLVYDEIKKTV 297
 Db 250 DILKNTLDCAKKTIQNEGMSAFKGLSNVFRGTGALVAYIDEIQKL 300

RESULT 13

T15206

hypothetical protein W02D3.6 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 21-Jan-2000

C:Accession: T15206

R:Le, T.; Weinstock, L.; Rijkkin, L.

submitted to the EMBL data library, May 1997

A:Description: The sequence of C. elegans cosmid W02D3.

A:Reference number: Z18308

A:Accession: T15206

A>Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-300 <LETT>

A:Cross-references: EMBL:AF003141; NID:g2088732; PID:g2088738; PIDN:AA54179.1; GSPDB:GA

A:Experimental source: strain Bristol N2; clone W02D3

C:Genetics:

A:Gene: CESP:W02D3.6

A:Map position: 1

C:Superfamily: ADP, ATP carrier protein; ADP, ATP carrier protein repeat homology

F;9-103/Domain: ADP, ATP carrier protein repeat homology <ACR>

Query Match 64.7%; Score 1005.5; DB 2; Length 300;

Best Local Similarity 66.0%; Pred. No. 2,2e-83;

Matches 192; Conservative 40; Mismatches 56; Indels 3; Gaps 2;

QY 8 FLKDFLAGAANAASKTAVAPIERVKLLQVOHASKOISAEKQYKGIIDCVIRPKQGF 67
 Db 12 FLIDVLAGSCTAAASKTAVAPIERVKLLQVOHASKOISAEKQYKGIIDCVIRPKQGF 71
 QY 68 LSFWRGNLANVIRFPTQALNFAFKDKYKQLFLGVDVRRHKOFRMYFAGNLAGSGAAGATS 127
 Db 72 AAFMRGNLANVIRFPTQALNFAFKDKYKQLFLGVDVRRHKOFRMYFAGNLAGSGAAGATS 131
 QY 128 LCFEYPLDFAFRTLRADVGRRAQREFHGLDCCIIFKFSQDGLKGLYOGFVNSVOGIIIR 187
 Db 132 LCFEYPLDFAFRTLRADVGRRAQREFHGLDCCIIFKFSQDGLKGLYOGFVNSVOGIIIR 191
 QY 188 AAFEGYVDIAKGM-L-PDPKRVHIFVSMIAQSTAVAGLLSYFEDYVRRMMQSGRKA 246
 Db 192 AAFEGMDTAKMVFASDQKLNFEPAAGIAQVTVGSGIISYPMDYVRRMMQSGRKA-- 249
 QY 247 DIWYTGVDQMRKIAKDEGAKAFKGMNSVLRGMSGAFVLVYDEIKKTV 297
 Db 250 DILKNTLDCAKKTIQNEGMSAFKGLSNVFRGTGALVAYIDEIQKL 300

RESULT 14

A41677

ADP, ATP carrier protein - Chlorella kessleri

C:Species: Chlorella kessleri

C:Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 20-Aug-1999

C:Accession: A41677
 R:Halgarth, C.; Sauer, N.; Tanner, W.
 J. Biol. Chem. 266, 24044-24047, 1991
 A:Title: Glucose increases the expression of the ADP/ATP translocator and the glycera
 A:Reference number: A41677; MUID:92084708; PMID:1748677
 A:Accession: A41677
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-339 <HLL>
 A:Cross-references: GB:M76669; NID:g516596; PIDN:AAA33027.1; PID:g516597
 C:Superfamily: ADP, ATP carrier protein; ADP, ATP carrier protein repeat homology
 F;36-134/Domain: ADP, ATP carrier protein repeat homology <ACP1>
 F;144-235/Domain: ADP, ATP carrier protein repeat homology <ACP2>
 F;241-329/Domain: ADP, ATP carrier protein repeat homology <ACP3>

Query Match 62.7%; Score 973.5; DB 2; Length 339;

Best Local Similarity 65.3%; Pred. No. 2e-80;

Matches 192; Conservative 30; Mismatches 65; Indels 7; Gaps 4;

QY 7 SFLKDFLAGAANAASKTAVAPIERVKLLQVOHASKOISAEK-QYKGIIDCVIRPK 64
 Db 40 AFYKDLAAGCTAGAIKSTAVAPIERVKLLQVDSNMISGVPRRTGIVNCFVRSSE 99
 QY 65 QGFLSEWRGNLANVIRFPTQALNFAFKDKYKQLFLGVDVRRHKOFRMYFAGNLAGSGAAG 124
 Db 100 QGVASEWRGNLANVIRFPTQALNFAFKDKYKQLFLGVDVRRHKOFRMYFAGNLAGSGAAG 158
 QY 125 ATSLCFYPLDFAFRTLRADVGRRAQREFHGLDCCIIFKFSQDGLKGLYOGFVNSVOGII 184
 Db 159 AGSLIYPLDFAFRTLRADVGRRAQREFHGLDCCIIFKFSQDGLKGLYOGFVNSVOGII 218
 QY 185 IYRAAYGVYDIAKGM-L-PDPKRVHIFVSMIAQSTAVAGLLSYFEDYVRRMMQSGR 243
 Db 219 VYNGAYGGLDFAKGVLFKDEKRTANFAKAAVAGVLAGVLSYFEDYVRRMMQSGR-- 276
 QY 244 KGADIMTGTVDQMRKIAKDEGAKAFKGMNSVLRGMSGAFVLVYDEIKKTV 297
 Db 277 -GGEROYNGYTIQDCMRKVAQOEGMFAFKGMNSVLRGMSGAFVLVYDEIKKTV 329

RESULT 15

S51132

ADP, ATP carrier protein - malaria parasite (Plasmodium falciparum)

N:Alternate names: ADP/ATP transporter

C:Species: Plasmodium falciparum

C:Date: 07-May-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jun-2000

C:Accession: S68993; S51132

R:Halgin, J.; Jauregui, G.

Eur. J. Biochem. 228, 86-91, 1995

A:Title: Molecular characterisation of the ADP/ATP-transporter cDNA from the human ma

A:Reference number: S68993; MUID:95188918; PMID:7883016

A:Accession: S68993

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-301 <HAT>

A:Cross-references: EMBL:X83551; NID:g623334; PIDN:CA58541.1; PID:g623335

C:Superfamily: ADP, ATP carrier protein; ADP, ATP carrier protein repeat homology

F;6-103/Domain: ADP, ATP carrier protein repeat homology <ACP1>

F;112-203/Domain: ADP, ATP carrier protein repeat homology <ACP2>

F;209-301/Domain: ADP, ATP carrier protein repeat homology <ACP3>

Query Match 58.2%; Score 904.5; DB 2; Length 301;

Best Local Similarity 58.3%; Pred. No. 3.1e-74;

Matches 172; Conservative 48; Mismatches 70; Indels 5; Gaps 4;

QY 7 SFLKDFLAGAANAASKTAVAPIERVKLLQVOHASKOISAEK-QYKGIIDCVIRPK 64
 Db 8 NFAADFLMGISAIKSTVTPIERVKMLQVDSNIPKISGVPRRTGIVNCFVRSSE 67
 QY 65 QGFLSEWRGNLANVIRFPTQALNFAFKDKYKQLFLGVDVRRHKOFRMYFAGNLAGSGAAG 124

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Db      68  QGVLSLMRGVANYIRYPTQAFNFAFKDYFNIF-PRYDONTDFSKFFCVNIIISGATAG 126
QY      125  ATSLCFVYPLDFAFRLADYGRRAQREFFHIGDCIIRKFKSDGRLGYGFNVSVGGII 184
      127  AISLIIVYPLDFARTRRLASDYGKDRQFTGIFDCLAKIKOTGLSLXSGFVSVTGII 186
QY      185  IYRAAYEGVYDTAKGML-PDPKNVHIYVSMIAQSVTAAGLLSYFPDTPVRRMMQSGR 243
      187  VYRGSYFGLYDSAKALLFTNDKNTNIVLKNVAQSVTIIAGLISYFPDTPVRRMMQSGR 246
Db
QY      244  KG-ADIMTGVDCARKIAKDEGAKAFKGAAMSNVLRMGCAFVLYDEIKKIY 297
      247  KGKEIIQYKNTIDCWIKILRNEGFKFGAMANYIRGAGALVLYFYDELOKLI 301

```

Search completed: August 28, 2003, 19:43:17
 Job time : 21.6204 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 28, 2003, 19:28:06 ; Search time 11.9731 Seconds

(without alignments)
1166.524 Million cell updates/sec

Title: US-09-811-132-31

Perfect score: 1553

Sequence: 1 MGDHMSFLKDFLAGAVAA.....LRGNGAFVLYDEIKRYV 297

Scoring table: BIOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues
Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match length | ID | Description |
|------------|--------|--------------------|-------|-------------|
| 1 | 1526.5 | 98.3 | 298 1 | ADP1_HUMAN |
| 2 | 1466.5 | 94.4 | 298 1 | ADP1_RAT |
| 3 | 1463.5 | 94.2 | 298 1 | ADP1_MOUSE |
| 4 | 1453.5 | 93.6 | 297 1 | ADP1_BOVIN |
| 5 | 1408.5 | 90.7 | 298 1 | ADP2_MOUSE |
| 6 | 1407.5 | 90.6 | 298 1 | ADP2_MOUSE |
| 7 | 1398.5 | 90.1 | 298 1 | ADP2_MOUSE |
| 8 | 1385.5 | 88.2 | 298 1 | ADP2_MOUSE |
| 9 | 1380.5 | 88.9 | 298 1 | ADP3_HUMAN |
| 10 | 1241 | 79.9 | 299 1 | ADT3_BOVIN |
| 11 | 1162.5 | 74.9 | 301 1 | ADT_DROME |
| 12 | 973.5 | 63.7 | 339 1 | ADT_CHICK |
| 13 | 770.5 | 49.6 | 308 1 | ADT_CHICK |
| 14 | 756.5 | 48.7 | 387 1 | ADT1_MAIZE |
| 15 | 752.5 | 48.5 | 322 1 | ADT1_MAIZE |
| 16 | 752.5 | 48.5 | 386 1 | ADT1_MAIZE |
| 17 | 751.5 | 48.4 | 387 1 | ADT1_MAIZE |
| 18 | 751.5 | 48.4 | 387 1 | ADT1_MAIZE |
| 19 | 746 | 48.0 | 381 1 | ADP2_MOUSE |
| 20 | 744.5 | 47.9 | 386 1 | ADP1_MOUSE |
| 21 | 742.5 | 47.8 | 331 1 | ADP1_MOUSE |
| 22 | 740 | 47.6 | 386 1 | ADP1_MOUSE |
| 23 | 736 | 47.4 | 307 1 | ADP2_MOUSE |
| 24 | 734 | 47.3 | 318 1 | ADP2_MOUSE |
| 25 | 733.5 | 47.2 | 313 1 | ADP2_MOUSE |
| 26 | 731 | 47.1 | 305 1 | ADP2_MOUSE |
| 27 | 729 | 46.9 | 305 1 | ADT1_MAIZE |
| 28 | 728.5 | 46.9 | 331 1 | ADT1_MAIZE |
| 29 | 718.5 | 46.3 | 309 1 | ADP1_MOUSE |
| 30 | 302.5 | 19.5 | 678 1 | ADP1_MOUSE |
| 31 | 300.5 | 19.3 | 330 1 | ADP1_MOUSE |
| 32 | 296.5 | 19.1 | 565 1 | ADP1_MOUSE |
| 33 | 296.5 | 19.1 | 702 1 | ADP1_MOUSE |

| | | | | | |
|----|-------|------|-------|------------|--------------------|
| 34 | 296 | 19.1 | 588 1 | CMC2_CAEEL | Q20799 caenorhabd1 |
| 35 | 295 | 19.0 | 322 1 | GDC_RAT | P16261 rattus norv |
| 36 | 292.5 | 18.8 | 307 1 | ODC2_YEAST | O99297 saccharomyc |
| 37 | 292 | 18.8 | 332 1 | GDC_HUMAN | P16260 homo sapien |
| 38 | 291 | 18.7 | 675 1 | CMC2_HUMAN | O99250 homo sapien |
| 39 | 280 | 18.0 | 315 1 | MT_HUMAN | O99251 homo sapien |
| 40 | 279.5 | 18.0 | 676 1 | CMC2_MOUSE | O99252 mus musculu |
| 41 | 270.5 | 17.4 | 315 1 | SA18_HUMAN | O99253 mus musculu |
| 42 | 267.5 | 17.2 | 325 1 | UCP5_MOUSE | O99254 mus musculu |
| 43 | 266.5 | 17.2 | 310 1 | UCP5_MOUSE | O99255 mus musculu |
| 44 | 265.5 | 17.1 | 325 1 | UCP5_MOUSE | O99256 mus musculu |
| 45 | 263.5 | 17.0 | 695 1 | CMC1_DROME | O99257 drosophila |

ALIGNMENTS

| RESULT 1 | ID | ADP1_HUMAN | STANDARD: | PRT: | 298 AA. |
|----------|---|-----------------------------------|-----------|------|---------|
| AC | P12235 | | | | |
| DT | 01-OCT-1989 | (Rel. 12, Created) | | | |
| DT | 01-NOV-1990 | (Rel. 16, Last sequence update) | | | |
| DT | 15-SEP-2003 | (Rel. 42, Last annotation update) | | | |
| DE | ADP, ATP carrier protein, heart/skeletal muscle isoform T1 (ADP/ATP translocase 1) (Adenine nucleotide translocator 1) (ANT 1). | | | | |
| GN | SLC25A4 OR ANT1. | | | | |
| OS | Homo sapiens (Human). | | | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo. | | | | |
| OX | NCBI_TaxID=9606; | | | | |
| RP | SEQUENCE FROM N.A. | | | | |
| RX | MEDLINE=89236396; PubMed=2541251; | | | | |
| RA | Cozens A.L., Runswick M.J., Walker J.E.; | | | | |
| RT | "DNA sequences of two expressed nuclear genes for human mitochondrial ADP/ATP translocase."; | | | | |
| RL | J. Mol. Biol. 206:261-280(1989). | | | | |
| RL | [2] | | | | |
| RP | SEQUENCE FROM N.A. | | | | |
| RX | MEDLINE=89340499; PubMed=2547778; | | | | |
| RA | Li K., Warner C.K., Hodge J.A., Minoshima S., Kudoh J.; | | | | |
| RT | Fukuyama R., Maekawa M., Shimizu Y., Shimizu N., Wallace D.C.; | | | | |
| RT | "A human muscle adenine nucleotide translocator gene has four exons, is located on chromosome 4, and is differentially expressed."; | | | | |
| RL | J. Biol. Chem. 264:13998-14004(1989). | | | | |
| RL | [3] | | | | |
| RP | SEQUENCE FROM N.A. | | | | |
| RX | MEDLINE=88041149; PubMed=2823266; | | | | |
| RA | Neckelmann N., Li K., Wade R.P., Shuster R., Wallace D.C.; | | | | |
| RT | "CDNA sequence of a human skeletal muscle ADP/ATP translocator: Jack of a leader peptide, divergence from a fibroblast translocator cDNA, and coevolution with mitochondrial DNA genes."; | | | | |
| RL | Proc. Natl. Acad. Sci. U.S.A. 84:7580-7584(1987). | | | | |
| RL | [4] | | | | |
| RP | SEQUENCE FROM N.A. | | | | |
| RC | TISSUE-EYE: | | | | |
| RA | MEDLINE=22388257; PubMed=12477932; | | | | |
| RA | Strausberg R.L., Reingold E.A., Grouse L.H., Derge J.C.; | | | | |
| RA | Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.; | | | | |
| RA | Altschul S.F., Zeeberg B., Buetow K.H., Scheffer C.F., Bhat N.K.; | | | | |
| RA | Hopkins R.E., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.; | | | | |
| RA | Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.; | | | | |
| RA | Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.; | | | | |
| RA | Brownstein M.T., Usdin T.B., Toshiyuki S., Carninci P., Prange C.; | | | | |
| RA | Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.; | | | | |
| RA | Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.; | | | | |
| RA | Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hults S.W.; | | | | |
| RA | Villaion D.K., Muzny E., Sodergren E.J., Lu X., Gibbs R.A.; | | | | |
| RA | Fahy J., Helton E., Kertman M., Madan A., Rodrigues S., Sanchez A.; | | | | |
| RA | Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.; | | | | |
| RA | Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.; | | | | |
| RA | Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.; | | | | |

RA Butterfield V.S.N., Krzywinski M.I., Skalska U., Smalins D.E.,
 RA Schnerich A., Schein J.E., Jones S.J.M., Maria M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length
 RT human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 RN [5]
 RC SEQUENCE OF 1-37 FROM N.A.
 RC TISSUE-LIVER;
 RA MEDLINE=88124845; PubMed=2829183;
 RA Houldsworth J., Attardi G.;
 RT "Two distinct genes for ADP/ATP translocase are expressed at the mRNA
 RT level in adult human liver.";
 RL Proc. Natl. Acad. Sci. U.S.A. 85:377-381(1988).
 RN [6]
 RP VARIANTS PEO PRO-114 AND MET-289.
 RA MEDLINE=40385067; PubMed=10926541;
 RA Rukenen J., Juselius J.K., Tirttilä V., Kyttälä A., Zeviani M.,
 RA Comi G.P., Kerenen J., Peltonen L., Sommalainen A.;
 RT "Role of adenine nucleotide translocator 1 in mtDNA maintenance.";
 RL Science 289:782-785(2000).
 CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
 CC MITOCHONDRIAL INNER MEMBRANE.
 CC -1- SUBUNIT: Homodimer.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
 CC inner membrane.
 CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
 CC -1- DISEASE: Defects in SLC25A4 are a cause of autosomal dominant
 CC progressive external ophthalmoplegia with various mitochondrial
 CC DNA deletions (PEO). Patients with PEO have mitochondrial
 CC myopathy, progressive external ophthalmoplegia, and other
 CC abnormalities associated with multiple different deletions of
 CC mitochondrial DNA.
 CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
 CC -----
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 CC -----
 DR EMBL: J029966; AAA61223.1; -;
 DR EMBL: J03593; AAA36751.1; -;
 DR EMBL: J04982; AAA51736.1; -;
 DR EMBL: BC008664; AAH08664.1; -;
 DR PIR: A44778; A44778.
 DR Genew: HGNC:10990; SLC25A4.
 DR MIM: 103220; -;
 DR MIM: 157640; -;
 DR GO: GO:0005887; C: integral to plasma membrane; TAS.
 DR GO: GO:0005739; C: mitochondrion; TAS.
 DR GO: GO:0015207; F: adenine transporter activity; TAS.
 DR GO: GO:0006091; F: energy pathways; TAS.
 DR GO: GO:0000002; P: mitochondrial genome maintenance; TAS.
 DR GO: GO:000632; P: small molecule transport; TAS.
 DR InterPro: IPR002067; MLC_carrier.
 DR InterPro: IPR002030; MLC_uncoupling.
 DR InterPro: IPR001993; Mitoch_carrier.
 DR Pfam: PF00153; mito_carr; 3.
 DR Pfam: PRO0926; MITOCARRIER.
 DR PRINTS: PRO0784; MITOCOUPLING.
 DR PROSITE: PS00215; MITOCH_CARRIER; 3.
 KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
 KW Multigene family; Disease mutation.
 FT TRANSMEM 12 29 1 (POTENTIAL).
 FT TRANSMEM 73 91 2 (POTENTIAL).
 FT TRANSMEM 117 134 3 (POTENTIAL).
 FT TRANSMEM 176 195 4 (POTENTIAL).
 FT TRANSMEM 214 231 5 (POTENTIAL).
 FT TRANSMEM 273 291 6 (POTENTIAL).
 FT REPEAT 1 110 1.
 FT REPEAT 111 208 2.

FT REPEAT 209 298 3.
 FT VARIANT 114 114 A -> P (IN PEO).
 FT VARIANT 289 289 /FTID-VAR_012111.
 FT VARIANT 289 289 V -> M (IN PEO).
 FT VARIANT 289 289 /FTID-VAR_012112.
 FT CONFLICT 16 16 G -> A (IN REF. 3).
 FT CONFLICT 147 149 KGA -> RR (IN REF. 3).
 FT CONFLICT 227 227 V -> L (IN REF. 3).
 SQ SEQUENCE 298 AA; 33064 MW; 59F0DFACAE7CEBB CRC64;
 Query Match 98.3%; Score 1526.5; DB 1; Length 298;
 Best Local Similarity 98.3%; Pred. No. 2e-129; 2; Indels 1; Gaps 1;
 Matches 293; Conservative 2; Mismatches 2;
 QY 1 MGDHANSFLKDFLAGVAVAASVSTAAPLIERVLLQVQHASQISAERKQKIIDCVAR 60
 DB 1 MGDHANSFLKDFLAGVAVAASVSTAAPLIERVLLQVQHASQISAERKQKIIDCVAR 60
 QY 61 IPKEQGFSLFWKRNLANVIRFPQALNFAFKRYQQLGVDYRKQKQRRYRAGNLASG 120
 DB 61 IPKEQGFSLFWKRNLANVIRFPQALNFAFKRYQQLGVDYRKQKQRRYRAGNLASG 120
 QY 121 GAAGATSLCFVPLDFAPRLADVGR-RAQREPHGIGDCITIKFSDGLRGLYOGFPNV 179
 DB 121 GAAGATSLCFVPLDFAPRLADVGR-RAQREPHGIGDCITIKFSDGLRGLYOGFPNV 180
 QY 180 VQGIITRYRAVFCGYDTAKGMLDPKRNHIFVSMIAQSVTAAGLSYFPDTRRRMM 239
 DB 181 VQGIITRYRAVFCGYDTAKGMLDPKRNHIFVSMIAQSVTAAGLSYFPDTRRRMM 240
 QY 240 QSGRKADIVYITGVDCWKRIADGAKAFKQKAMSIVLRGKGAVLYLYDEIKRYV 297
 DB 241 QSGRKADIVYITGVDCWKRIADGAKAFKQKAMSIVLRGKGAVLYLYDEIKRYV 298
 RESULT 2
 ADL1_RAT STANDARD; PRT; 298 AA.
 ID ADL1_RAT
 AC 005962;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE ADP/ATP carrier protein, heart/skeletal muscle isoform T1 (ADP/ATP
 DE translocase 1) (Adenine nucleotide translocator 1) (ANT 1).
 GN SLC25A4 OR ANT1.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN-Sprague-Dawley, and Wistar; TISSUE-Heart, and Liver;
 RX MEDLINE=94002161; PubMed=8399300;
 RA Shiohara Y., Kamida M., Yamazaki N., Terada H.;
 RT "Isolation and characterization of cDNA clones and a genomic clone
 RT encoding rat mitochondrial adenine nucleotide translocator.";
 RL Biochim. Biophys. Acta 1152:192-196(1993).
 CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
 CC MITOCHONDRIAL INNER MEMBRANE.
 CC -1- SUBUNIT: Homodimer.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
 CC inner membrane.
 CC -1- TISSUE SPECIFICITY: IN HEART, SKELETAL MUSCLE AND TO A LESSER
 CC EXTENT, IN BRAIN AND KIDNEY.
 CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
 CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
 CC -----
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or send an email to license@lsb-sib.ch.

CC EMBL: X61667; CAA43842.1; -
 DR EMBL: D12770; BAA02337.1; -
 DR PIR: I60173; I60173.
 DR InterPro: IPR002067; Mlt_carrier.
 DR InterPro: IPR002030; Mlt_uncoupling.
 DR Pfam: PF00153; mito_carrier_3.
 DR PRINTS: PR00926; MITOCARRIER.
 DR PRINTS: PR00784; MTUNCOUPLING.
 DR PROSITE: PS00215; MITOCH_CARRIER; 3.
 KM Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
 KM Multigene family.
 FT TRANSMEM 12 29 1 (POTENTIAL).
 FT TRANSMEM 73 91 2 (POTENTIAL).
 FT TRANSMEM 117 134 3 (POTENTIAL).
 FT TRANSMEM 176 195 4 (POTENTIAL).
 FT TRANSMEM 214 231 5 (POTENTIAL).
 FT TRANSMEM 273 291 6 (POTENTIAL).
 FT REPEAT 1 110 1.
 FT REPEAT 111 208 2.
 FT REPEAT 209 298 3.
 SQ SEQUENCE 238 AA; 32989 MW; 66704FF78C6BC320 CRC64;

Query Match 94.4%; Score 1466.5; DB 1; Length 298;
 Best Local Similarity 94.3%; Pred. No. 4.7e-124;
 Matches 281; Conservative 9; Mismatches 7; Indels 1; Gaps 1;

QY 1 MGDHMSLKPLAGAAVAASKTAADIERVKLLQVHASKQISAKQYKGIIDCYVR 60
 1 GGDALSLKDFLGGAGIAASKTAADIERVKLLQVHASKQISAKQYKGIIDCYVR 60
 DB 61 IPKEGFLSPFRGNLANIYRFPYQALNFAFRKDKYKFLGVDHKGFWRFAGNLASG 120
 61 IPKEGFLSPFRGNLANIYRFPYQALNFAFRKDKYKFLGVDHKGFWRFAGNLASG 120
 QY 121 GAAGATSLCFYVPLDFARTLADYGR-RAQREPHGLDCIIFKSGDLNGLYOGFNVS 179
 121 GAAGATSLCFYVPLDFARTLADYGR-RAQREPHGLDCIIFKSGDLNGLYOGFNVS 179
 DB 121 GAAGATSLCFYVPLDFARTLADYGR-RAQREPHGLDCIIFKSGDLNGLYOGFNVS 180
 121 GAAGATSLCFYVPLDFARTLADYGR-RAQREPHGLDCIIFKSGDLNGLYOGFNVS 180
 QY 180 VGGITTYAAAFGYVDYDAKGMPLPKNKHIFYSMMIAOSVAVAGLSTPDDYRRMM 239
 180 VGGITTYAAAFGYVDYDAKGMPLPKNKHIFYSMMIAOSVAVAGLSTPDDYRRMM 239
 DB 181 VGGITTYAAAFGYVDYDAKGMPLPKNKHIFYSMMIAOSVAVAGLSTPDDYRRMM 240
 181 VGGITTYAAAFGYVDYDAKGMPLPKNKHIFYSMMIAOSVAVAGLSTPDDYRRMM 240
 QY 240 QSGRGADIMTGVDCRKTAKDEGAKAFKGAAMSVNLRGGAFFVLYLDEIKKYV 297
 240 QSGRGADIMTGVDCRKTAKDEGAKAFKGAAMSVNLRGGAFFVLYLDEIKKYV 297
 DB 241 QSGRGADIMTGVDCRKTAKDEGAKAFKGAAMSVNLRGGAFFVLYLDEIKKYV 298
 241 QSGRGADIMTGVDCRKTAKDEGAKAFKGAAMSVNLRGGAFFVLYLDEIKKYV 298

RESULT 3
 ADP1_MOUSE STANDARD: PRT: 298 AA.

AC P48962; Q62164; -
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 28-FEB-2003 (Rel. 41, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE ADP_Arp carrier protein, heart/skeletal muscle isoform T1 (ADP/ATP translocase 1) (Adenine nucleotide translocator 1) (ANT 1) (MANC1).
 GN SL2554 OR ANT1 OR ANCL.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclerognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RX MEDLINE=97059403; PubMed=8903724;
 RA Ellison J.W., Li X., Francke U., Shapiro L.J.;
 RT "Rapid evolution of human pseudautosomal genes and their mouse homologs.";
 RL Mann. Genome 7:25-30(1996).
 RN [2]

RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/c; TISSUE=Muscle;
 RA Laplace C., Costet P.;
 RL Submitted (SEP-1993) to the EMBL/Genbank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RA Levy S.E., Chen Y.-S., Graham B.H., Wallace D.C.;
 RT "Expression and sequence analysis of the mouse adenine nucleotide translocase 1 and 2 genes.";
 RL Submitted (Mar-2000) to the EMBL/Genbank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE=EYE;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Strassberg R.L., Pelngold E.A., Grouse L.H., Derge J.G.,
 RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
 RA Altschul S.F., Zeeberg B., Buelow K.H., Schaefer C.F., Blat N.K.,
 RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
 RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
 RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
 RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
 RA Rana S.S., Loguella N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
 RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
 RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
 RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
 RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
 RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
 RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
 RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
 RA Bottingfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E.,
 RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences.";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE MITOCHONDRIAL INNER MEMBRANE.
 CC -1- SUBUNIT: Homodimer.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial inner membrane.
 CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
 CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
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CC EMBL: U27315; AAC52837.1; -
 DR EMBL: X74510; CAA52616.1; -
 DR EMBL: AF240002; AAF64470.1; -
 DR EMBL: BC003791; AA03791.1; -
 DR EMBL: BC026925; AA026925.1; -
 DR PIR: S37210; S37210.
 DR MGD: MGI:1353495; SL2554.
 DR InterPro: IPR002067; Mlt_carrier.
 DR InterPro: IPR002030; Mlt_uncoupling.
 DR InterPro: IPR001993; Mitoch_carrier.
 DR Pfam: PF00153; mito_carrier_3.
 DR PRINTS: PR00926; MITOCARRIER.
 DR PRINTS: PR00784; MTUNCOUPLING.
 DR PROSITE: PS00215; MITOCH_CARRIER; 3.
 KM Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
 KM Multigene family.
 FT TRANSMEM 12 29 1 (POTENTIAL).
 FT TRANSMEM 73 91 2 (POTENTIAL).
 FT TRANSMEM 117 134 3 (POTENTIAL).
 FT TRANSMEM 176 195 4 (POTENTIAL).
 FT TRANSMEM 214 231 5 (POTENTIAL).
 FT TRANSMEM 273 291 6 (POTENTIAL).
 FT REPEAT 1 110 1.

```

FT REPEAT      111 208 2.
FT REPEAT      209 298 3.
FT CONFLICT    136 136 F -> L (IN REF. 1).
SQ SEQUENCE    298 AA; 32904 MW; 3A849FEAB0981462 CRC64;

Query Match
Best Local Similarity 94.08; Score 1463.5; DB 1; Length 298;
Matches 280; Conservative 10; Mismatches 7; Indels 1; Gaps 1;

QY 1 MGDHMSFLKDFLAGAANAASKTAVAPIERVKLLLOVHASKQISAERKQYGIIDCVVR 60
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 1 MGDALSLKDFLAGIAAASKTAVAPIERVKLLLOVHASKQISAERKQYGIIDCVVR 60
QY 61 IPRKQGLSFWKRGLANVIRFPQALNFAFKKQYKQFLGCVDRHKOFRYFAGNLSAG 120
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 61 IPRKQGLSFWKRGLANVIRFPQALNFAFKKQYKQFLGCVDRHKOFRYFAGNLSAG 120
QY 121 GAAGATSLCFYVPDFAFRTRLAADVGR-RAOREFHGLDCCIIRKFKSDGLRGVYGFNVS 179
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 121 GAAGATSLCFYVPDFAFRTRLAADVGR-RAOREFHGLDCCIIRKFKSDGLRGVYGFNVS 180
QY 180 VOGIIIRAAVFGVYDFAKGMPLDPKKNVHIFVSMIAQSVYAVAGLSYFEDTVRRMM 239
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 181 VOGIIIRAAVFGVYDFAKGMPLDPKKNVHIFVSMIAQSVYAVAGLSYFEDTVRRMM 240
QY 240 QSGRKADIMYTGTVDCWKRIAKDEGAKAFKGAWSNVLRGKGAFVLYLYDEIKKYV 297
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 241 QSGRKADIMYTGTVDCWKRIAKDEGAKAFKGAWSNVLRGKGAFVLYLYDEIKKYV 298

RESULT 4
ADT1_BOVIN STANDARD; PRT; 297 AA.
AC P02722;
DT 21-JUL-1986 (Rel. 01, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE ADP/ATP carrier protein, heart isoform T1 (ADP/ATP translocase 1)
DE (Adenine nucleotide translocator 1) (ANT 1).
GN SLC25A4 OR ANT1.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID:9913;
RN [1]
RP MEDLINE-89229093; PubMed-2540808;
RA Powell S.J., Medd S.M., Runswick M.J., Walker J.E.;
RT "Two bovine genes for mitochondrial ADP/ATP translocase expressed
RT differences in various tissues.";
RL Biochemistry 28:866-873(1989).
RN [2]
RP MEDLINE-82188267; PubMed-7076130;
RA Aquila H., Mista D., Eulitz M., Klingenberg M.;
RT "Complete amino acid sequence of the ADP/ATP carrier from beef heart
RT mitochondria.";
RL Hoppe-Seyler's Z. Physiol. Chem. 363:345-349(1982).
RN [3]
RP MEDLINE-6295775; PubMed-3017341;
RA Rasmussen U.B., Wohlb H.;
RT Bovine cardiac mitochondrial ADP/ATP-carrier: two distinct mRNAs and
RT an unusually short 3'-noncoding sequence.";
RL Biochem. Biophys. Res. Commun. 138:850-857(1986).
CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
CC MITOCHONDRIAL INNER MEMBRANE.
CC -1- SUBUNIT: Homodimer.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC inner membrane.
CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.

```

```

CC -----
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CC or send an email to license@isb.sib.ch).
CC -----
DR EMBL; M13783; AAA30363.1; -
DR EMBL; M24102; AAA30768.1; -
DR PIR; A43646; XERO
DR InterPro; IPR002067; Mlt_carrier.
DR InterPro; IPR002030; Mlt_uncoupling.
DR InterPro; IPR001993; Mitoch_carrier.
DR Pfam; PF00153; mlt_carr; 3.
DR PRINTS; PR00926; MITOCARRIER.
DR PRINTS; PR00784; MTUNCOUPLING.
DR PROSITE; PS00215; MITOCH_CARRIER; 3.
KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
KW Multigene family; Methylation.
FT MOD_RES 0 1
FT INT_MET 0 0
FT MOD_RES 1 1 BLOCKED.
FT TRANSRES 51 51 METHYLATION (POTENTIAL).
FT TRANSRES 11 28 1 (POTENTIAL).
FT TRANSRES 72 90 2 (POTENTIAL).
FT TRANSRES 116 133 3 (POTENTIAL).
FT TRANSRES 175 194 4 (POTENTIAL).
FT TRANSRES 213 230 5 (POTENTIAL).
FT TRANSRES 272 290 6 (POTENTIAL).
FT REPEAT 1 110 1.
FT REPEAT 111 207 2.
FT REPEAT 208 297 3.
SQ SEQUENCE 297 AA; 32836 MW; A582D3C4A40AE848 CRC64;

Query Match
Best Local Similarity 93.64; Score 1453.5; DB 1; Length 297;
Matches 280; Conservative 7; Mismatches 8; Indels 1; Gaps 1;

QY 3 DHAMSFLLKDFLAGAANAASKTAVAPIERVKLLLOVHASKQISAERKQYGIIDCVVRIP 62
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 2 DQALSLKDFLAGAANAASKTAVAPIERVKLLLOVHASKQISAERKQYGIIDCVVRIP 61
QY 63 KEQGLSFWKRGLANVIRFPQALNFAFKKQYKQFLGCVDRHKOFRYFAGNLSAG 122
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 62 KEQGLSFWKRGLANVIRFPQALNFAFKKQYKQFLGCVDRHKOFRYFAGNLSAG 121
QY 123 AGATSLCFYVPDFAFRTRLAADVGR-RAOREFHGLDCCIIRKFKSDGLRGVYGFNVSQ 181
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 122 AGATSLCFYVPDFAFRTRLAADVGR-RAOREFHGLDCCIIRKFKSDGLRGVYGFNVSQ 181
QY 182 GIITIRAAVFGVYDFAKGMPLDPKKNVHIFVSMIAQSVYAVAGLSYFEDTVRRMMMS 241
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 182 GIITIRAAVFGVYDFAKGMPLDPKKNVHIFVSMIAQSVYAVAGLSYFEDTVRRMMMS 241
QY 242 GRRGADIMYTGTVDCWKRIAKDEGAKAFKGAWSNVLRGKGAFVLYLYDEIKKYV 297
   | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | | |
DB 242 GRRGADIMYTGTVDCWKRIAKDEGAKAFKGAWSNVLRGKGAFVLYLYDEIKKYV 297

RESULT 5
ADT2_MOUSE STANDARD; PRT; 298 AA.
AC P51881; Q61311;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE ADP/ATP carrier protein, fibroblast isoform (ADP/ATP translocase 2)
DE (Adenine nucleotide translocator 2) (ANT 2).
GN SLC25A5 OR ANT2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniala; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

```

OX NCBI_TaxId=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RX MEDLINE=97059403; PubMed=8903724;
 RA Ellison J.W., Li X., Francke U., Shapiro L.J.;
 RT "Rapid evolution of human pseudautosomal genes and their mouse
 homologs.";
 RL Mamm. Genome 7:25-30(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Skeletal muscle;
 RA Sheldon J.G.;
 RL Thesis (1995), University of Cambridge, U.K.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=129/Sv;
 RA Coster P., Laplace C.;
 RL Submitted (FEB-1993) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP REVISIONS.
 RA Laplace C.;
 RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=20432087; PubMed=10974536;
 RA Levy S.E., Chen Y.-S., Graham B.H., Wallace D.C.;
 RT "Expression and sequence analysis of the mouse adenine nucleotide
 translocase 1 and 2 genes.";
 RL Gene 254:57-66(2000).
 CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
 CC MITOCHONDRIAL INNER MEMBRANE.
 CC -1- SUBUNIT: Homodimer.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
 CC inner membrane.
 CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
 CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
 CC -----
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 CC -----
 DR EMBL: U27316; AAC52838.1; -
 DR EMBL: U10404; AAI19009.1; -
 DR EMBL: X70847; CAA50196.1; -
 DR EMBL: AF240003; AAF64471.1; -
 DR MGI: 1353496; SLC25a5.
 DR InterPro: IPR002067; Mlt_carrier.
 DR InterPro: IPR002030; Mitoch_carrier.
 DR InterPro: IPR001993; Mitoch_carrier.
 DR Pfam: PF00153; mito_carr; 3.
 DR PRINTS: PR00926; MITOCARRIER.
 DR PRINTS: PR00784; MTUNCOUPLING.
 DR PROSITE: PS00215; MITOCH_CARRIER; 3.
 KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
 KM Multigene family.
 FT TRANSMEM 12 29 1 (POTENTIAL).
 FT TRANSMEM 73 91 2 (POTENTIAL).
 FT TRANSMEM 117 134 3 (POTENTIAL).
 FT TRANSMEM 176 195 4 (POTENTIAL).
 FT TRANSMEM 214 231 5 (POTENTIAL).
 FT TRANSMEM 273 291 6 (POTENTIAL).
 FT REPEAT 1 111 1.
 FT REPEAT 112 208 2.
 FT REPEAT 209 298 3.
 SQ SEQUENCE 298 AA; 32931 MW; 0798E04B987EFE20 CRC64;
 Query Match 90.7%; Score 1408.5; DB 1; Length 298;
 Best Local Similarity 89.6%; Pred. No. 7,3e-119;

Matches 266; Conservative 17; Mismatches 13; Indels 1; Gaps 1;
 QY 1 MGDHWSFLKDLFAGVAAVAASKTAVAPLERKYLQVQHASKOISAEKQYKGIIDCVRR 60
 DB 1 MTDAAVSFAKDLGAGVAAVAAISKTNAPIERKLLQVQHASKOIRADQKGIIDCVRR 60
 QY 61 IPKEGGLFSFWKGNLANVIRYPTQALNFAFDKTKQLFLGGVDRKQKWRFPAGLASC 120
 DB 61 IPKEGGLFSFWKGNLANVIRYPTQALNFAFDKTKQLFLGGVDRKQKWRFPAGLASC 120
 QY 121 GAAGATSLCEVYPLDPAFTRILADVGR-AOREFHGIGCIITKIEFSDGLGYGFNYS 179
 DB 121 GAAGATSLCEVYPLDPAFTRILADVGRKGAERFKGLGCLVTKYSDSIKGLYGFNYS 180
 QY 180 VGGIITRYAAYGVYDTAKGMLPDPKRVHIFVSMIAQSVTAVAGLSYFPDTRRRAM 239
 DB 181 VGGIITRYAAYGVYDTAKGMLPDPKRVHIFVSMIAQSVTAVAGLSYFPDTRRRAM 240
 QY 240 OSGRKGADIMYGFVDCWKRRIAKDEGAKAFPKGAMSNVLKMGCAFVLVLYDEIKKY 296
 DB 241 OSGRKGADIMYGTGLDCWKRRIARDEGSKAFKGMAMSNVLKMGCAFVLVLYDEIKKY 297
 RESULT 6
 ADT2_RAT STANDARD; PRT; 298 AA.
 AC 009073;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE ADP/ATP carrier protein, fibroblast isoform (ADP/ATP translocase 2)
 DE (Adenine nucleotide translocator 2) (ANT 2).
 GN SLC25A5 OR ANT2.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxId=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Sprague-Dawley; TISSUE=Liver;
 RX MEDLINE=94002161; PubMed=8399300;
 RA Shinhara Y., Kamada M., Yamazaki N., Terada H.;
 RT "Isolation and characterization of cDNA clones and a genomic clone
 RT encoding rat mitochondrial adenine nucleotide translocator.";
 RL Biochim. Biophys. Acta 1152:192-196(1993).
 CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
 CC MITOCHONDRIAL INNER MEMBRANE.
 CC -1- SUBUNIT: Homodimer.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
 CC inner membrane.
 CC -1- TISSUE SPECIFICITY: PRESENT IN KIDNEY, BRAIN, HEART, LIVER AND
 CC SKELETAL MUSCLE.
 CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
 CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
 CC -----
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 CC -----
 DR EMBL: D12771; BAA02238.1; -
 DR InterPro: IPR002067; Mlt_carrier.
 DR InterPro: IPR002030; Mlt_uncoupling.
 DR InterPro: IPR001993; Mitoch_carrier.
 DR Pfam: PF00153; mito_carr; 3.
 DR PRINTS: PR00926; MITOCARRIER.
 DR PRINTS: PR00784; MTUNCOUPLING.
 DR PROSITE: PS00215; MITOCH_CARRIER; 3.
 KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
 KM Multigene family.

```

FT TRANSMEM 12 29 1 (POTENTIAL).
FT TRANSMEM 73 91 2 (POTENTIAL).
FT TRANSMEM 117 134 3 (POTENTIAL).
FT TRANSMEM 176 195 4 (POTENTIAL).
FT TRANSMEM 214 231 5 (POTENTIAL).
FT TRANSMEM 273 291 6 (POTENTIAL).
FT REPEAT 1 111 1.
FT REPEAT 112 208 2.
FT REPEAT 209 298 3.
SQ SEQUENCE 298 AA; 32901 MW; 6A59204B987EEF35 CRC64;

Query Match 90.6%; Score 1407.5; DB 1; Length 298;
Best Local Similarity 89.6%; Pred. No. 9e-119;
Matches 266; Conservative 16; Mismatches 14; Indels 1; Gaps 1;

OY 1 MGDHMSFLKDFLAGAANAASKTAVAPIERVKLLLOVHASQISAQKQYKGIIDCVR 60
DB 1 MTDAVAASFADFLAGVAAAIKSTAVAPIERVKLLLOVHASQITADKQYKGIIDCVR 60
OY 61 IPKEQGLSFWRCNLAVIRYFPTQALNFAFKDKYKQFLGVDNRHQRFRYFAGNLASG 120
DB 61 IPKEQGLSFWRCNLAVIRYFPTQALNFAFKDKYKQIFLGVDNRHQRFRYFAGNLASG 120
OY 121 GAAGATSLCEVYPLDFARTLADYGR-AOREFHGLGDCIITKFKSDGLRGLYQGFNVS 179
DB 121 GAAGATSLCEVYPLDFARTLADYGRKAGAREFEKGLGDCIIVKIKYKSDGKGLYQGFNVS 180
OY 180 VOGIIIRAYAFGYVDFAKGMLPDPKRVHIFVSMINOSYAVAGLSTYFPDVRRRMM 239
DB 181 VOGIIIRAYAFGYVDFAKGMLPDPKRVHIFISMLNOSTYAVAGLSTYFPDVRRRMM 240
OY 240 QSGNRKADIMYGTGVDKWRITADEGAKAEFFKAGMSVNLGMSGAFVLYLDEIKKY 296
DB 241 QSGNRKADIMYGTGVDKWRITADEGAKAEFFKAGMSVNLGMSGAFVLYLDEIKKY 297

RESULT 7
ADT2_HUMAN STANDARD; PRT; 298 AA.
AC P05141; O43350;
DT 13-AUG-1987 (Rel. 05, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE ADP, ATP carrier protein, fibroblast isoform (ADP/ATP translocase 2)
GN (Adenine nucleotide translocator 2) (ANT 2).
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=90375457; PubMed=2168878;
RA Ka D.-H., Kagan J., Chen S.-T., Chang C.-D., Baserga R., Wurzel J.;
RT "The human fibroblast adenine nucleotide translocator gene. Molecular
RT cloning and sequence."
RL J. Biol. Chem. 265:16060-16063(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=87166056; PubMed=3031073;
RA Battini R., Ferrari S., Kaczmarek L., Calabretta B., Chen S.T.,
RA Baserga R.;
RT "Molecular cloning of a cDNA for a human ADP/ATP carrier which is
RT growth-regulated."
RL J. Biol. Chem. 262:4355-4358(1987).
RN [3]
RP SEQUENCE FROM N.A.
RA Chen C.N., Su Y., Baydayan P., Siruno A., Nagaraja R.,
RA Mazzarella R.A., Schllessinger D., Chen E.Y.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.

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RA Becker M., Graves T., Ozersky P.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE OF 47-298 FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=88124845; PubMed=2829183;
RA Houldsworth J., Attardi G.;
RT "Two distinct genes for ADP/ATP translocase are expressed at the mRNA
RT level in adult human liver."
RL Proc. Natl. Acad. Sci. U.S.A. 85:377-381(1988).
CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
CC MITOCHONDRIAL INNER MEMBRANE.
CC -1- SUBUNIT: Homodimer.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC inner membrane.
CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
CC
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DR EMBL: M57424; AAA51737.1; -
DR EMBL: J02683; AAA35579.1; -
DR EMBL: L78810; AAB39266.1; -
DR EMBL: AC004000; AAB96347.1; -
DR EMBL: J03591; AAA36749.1; -
DR PIR: A29132; A29132.
DR Genew: HGNC:10991; SLC25A5.
DR MIM: 300150; -
DR GO: GO:0005887; C: integral to plasma membrane; TAS.
DR GO: GO:0015207; F: adenine transporter activity; TAS.
DR GO: GO:0006832; P: small molecule transport; TAS.
DR InterPro: IPR002067; MLC_carrier.
DR InterPro: IPR002030; MLC_uncoupling.
DR InterPro: IPR001993; Mitoch_carrier.
DR Pfam: PF00153; mltc_carr; 3.
DR PRINTS: PRO0926; MITOCARRIER.
DR PRINTS: PRO0784; MTNCOUPLING.
DR PROSITE: PS00215; MITOCH_CARRIER; 3.
KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
KW Multigene family.
FT TRANSMEM 12 29 1 (POTENTIAL).
FT TRANSMEM 73 91 2 (POTENTIAL).
FT TRANSMEM 117 134 3 (POTENTIAL).
FT TRANSMEM 176 195 4 (POTENTIAL).
FT TRANSMEM 214 231 5 (POTENTIAL).
FT TRANSMEM 273 291 6 (POTENTIAL).
FT REPEAT 1 111 1.
FT REPEAT 112 208 2.
FT REPEAT 209 298 3.
FT CONFLICT 6 6 V -> L (IN REF. 2).
FT CONFLICT 66 66 G -> E (IN REF. 2).
FT CONFLICT 111 111 R -> L (IN REF. 4 AND 5).
FT CONFLICT 162 162 V -> G (IN REF. 5).
SQ SEQUENCE 298 AA; 32895 MW; F973C3AED92C49D3 CRC64;

Query Match 90.1%; Score 1398.5; DB 1; Length 298;
Best Local Similarity 88.9%; Pred. No. 5.8e-118;
Matches 264; Conservative 17; Mismatches 15; Indels 1; Gaps 1;

OY 1 MGDHMSFLKDFLAGAANAASKTAVAPIERVKLLLOVHASQISAQKQYKGIIDCVR 60
DB 1 MTDAVAASFADFLAGVAAAIKSTAVAPIERVKLLLOVHASQITADKQYKGIIDCVR 60
OY 61 IPKEQGLSFWRCNLAVIRYFPTQALNFAFKDKYKQFLGVDNRHQRFRYFAGNLASG 120
DB 61 IPKEQGLSFWRCNLAVIRYFPTQALNFAFKDKYKQIFLGVDNRHQRFRYFAGNLASG 120

```

| | | |
|-----|---|-----|
| 0Y | GAAGTATCCTFYPDFAETRLAADVAGR-AQDEPFLGBCIIRKIFPSDGLRGLYQSENNV | 179 |
| 121 | | |
| Db | GAAGTATCCTFYPDFAETRLAADVAGKGAEREERFGLGCLVAKYKSDIRKGLYQSENNV | 180 |
| 121 | | |
| 0Y | VQGIITVAAEYGVDTAKGMLPDKKNHIFPSWMAIOSVTAVAGLLSTVPDFVRRMM | 239 |
| 180 | | |
| Db | VQGIITVAAEYGVDTAKGMLPDKKNHIVISWMAIQVTVAAGLTSYVPDFVRRMM | 240 |
| 181 | | |
| 0Y | QSGRRGADIMTGVDFCDKRIKIDEGAKAFKGSNNVLRGAGAVLVLYDEIRKY | 296 |
| 240 | | |
| Db | QSGRRGADIMTGVDFCDKRIKIDEGAKAFKGSNNVLRGAGAVLVLYDEIRKY | 297 |
| 241 | | |

RESULT 8

| ID | ADP3 | HUMAN | STANDARD: | PRT: | 298 AA. |
|----|---|-----------------------------------|-----------|------|---------|
| AC | P12236 | G96CA49 | | | |
| DF | 01-Oct-1989 | (Rel. 12, Created) | | | |
| DT | 15-SEP-2003 | (Rel. 42, Last sequence update) | | | |
| DT | 15-SEP-2003 | (Rel. 42, Last annotation update) | | | |
| DE | ADP/ATP carrier protein, liver isoform T2 (ADP/ATP translocase 3) | | | | |
| DE | (Adenine nucleotide translocator 3) (ANT 3). | | | | |
| GN | SLC25A6 OR ANT3. | | | | |
| OS | Homo sapiens (Human). | | | | |
| OC | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; | | | | |
| OC | Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo. | | | | |
| OX | NCBI_Taxid=9606; | | | | |
| RP | [1] | | | | |
| RP | SEQUENCE FROM N.A. | | | | |
| RX | MEDLIN=89236396; PubMed=2541251; | | | | |
| RA | Cozens A.L., Rungsback M.J., Walker J.E.; | | | | |
| RT | "DNA sequences of two expressed nuclear genes for human mitochondrial | | | | |
| RT | ADP/ATP translocase."; | | | | |
| RL | J. Mol. Biol. 206:261-280(1989). | | | | |
| RN | [2] | | | | |
| RP | SEQUENCE FROM N.A. | | | | |
| RA | Zhou J., Yu W., Tang H., Mei G., Tsang Y.T.M., Bouck J., Gibbs R.A., | | | | |
| RA | Margolin J.F.; | | | | |
| RL | Submitted (JUL-2000) to the EMBL/Genbank/DBJ databases. | | | | |
| RN | [3] | | | | |
| RP | SEQUENCE FROM N.A. | | | | |
| RC | TISSUE=Brain, Cervix, Eye, and Lung; | | | | |
| RX | MEDLIN=22388257; PubMed=12477932; | | | | |
| RA | Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G., | | | | |
| RA | Klausner R.D., Collins F.S., Wagner L.H., Shenmen C.M., Schuler G.D., | | | | |
| RA | Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., | | | | |
| RA | Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., | | | | |
| RA | Datchenko L., Marusina K., Farmer A.F., Rubin G.M., Hong L., | | | | |
| RA | Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E., | | | | |
| RA | Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C., | | | | |
| RA | Raba S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J., | | | | |
| RA | Bosnak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., | | | | |
| RA | Ricardus S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Huiyk S.W., | | | | |
| RA | Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., | | | | |
| RA | Fahney J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A., | | | | |
| RA | Whiting M., Madan A., Young A.C., Shevchenko V., Bouffard G.G., | | | | |
| RA | Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., | | | | |
| RA | Butterfield Y.S.N., Krzywinski M.T., Skalska U., Smalins D.E., | | | | |
| RA | Schmerer A., Schein J.E., Jones S.J.M., Maira M.A.; | | | | |
| RT | "Generation and initial analysis of more than 15,000 full-length | | | | |
| RT | human and mouse cDNA sequences."; | | | | |
| RL | Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002). | | | | |
| RN | [4] | | | | |
| RP | SEQUENCE OF 36-298 FROM N.A. | | | | |
| RC | TISSUE=Liver; | | | | |
| RX | MEDLIN=88124845; PubMed=2829183; | | | | |
| RA | Houldsworth J., Attardi G.; | | | | |
| RT | "Two distinct genes for ADP/ATP translocase are expressed at the mRNA | | | | |
| RT | level in adult human liver."; | | | | |
| RL | Proc. Natl. Acad. Sci. U.S.A. 85:377-381(1988). | | | | |
| CC | -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE | | | | |
| CC | MITOCHONDRIAL INNER MEMBRANE. | | | | |

```

CC -1- SUBUNIT: Homodimer.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC inner membrane.
CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@sib-sib.ch).
CC -----
DR EMBL; J03592; AAA36750.1; -
DR EMBL; AY007135; AAG01998.1; -
DR EMBL; AY007295; AAG07295.1; -
DR EMBL; BC007850; AAH07850.1; -
DR EMBL; BC008737; AAH08737.1; -
DR EMBL; BC008935; AAH08935.1; -
DR EMBL; BC014775; AAH14775.1; -
DR PIR; S03894; S03894.
DR Genew; HGNC:10992; SLC25A6.
DR MIM; 300151; -
DR MIM; 403000; -
DR GO; GO:0005744; C:mitochondrial inner membrane translocase co. .; TAS.
DR GO; GO:0005471; F:ATP/ADP antiporter activity; NAS.
DR GO; GO:0006854; P:ATP/ADP exchange; TAS.
DR InterPro; IPR002067; Mlt_carrier.
DR InterPro; IPR002030; Mlt_uncoupling.
DR InterPro; IPR001993; Mitoch_carrier.
DR Pfam; PF00153; mltc_carr; 3.
DR PRINTS; PR00926; MITOCARRIER.
DR PRINTS; PR00784; MTUNCOUPLING.
DR PROSITE; PS00215; MITOCH_CARRIER; 3.
KW Mitochondrion; inner membrane; Repeat; Transmembrane; Transport;
KW Multigene family.
KW
FT TRANSMEM 12 29 1 (POTENTIAL).
FT TRANSMEM 73 91 2 (POTENTIAL).
FT TRANSMEM 117 134 3 (POTENTIAL).
FT TRANSMEM 176 195 4 (POTENTIAL).
FT TRANSMEM 214 231 5 (POTENTIAL).
FT TRANSMEM 273 291 6 (POTENTIAL).
FT REPEAT 1 100 1.
FT REPEAT 101 208 2.
FT REPEAT 209 298 3.
FT CONFLICT 105 108 S -> F (IN REF. 3; AAH14775).
FT CONFLICT 242 242 KHTQ -> RHA (IN REF. 4).
SQ SEQUENCE 298 AA; 32866 MW; 1B534E9F0E49672F CRC64;
Query Match 89.2%; Score 1385.5; DB 1; Length 298;
Best Local Similarity 87.2%; Pred. No. 8,4e-117;
Matches 260; Conservative 21; Mismatches 16; Indels 1; Gaps 1;
QY 1 MGDHAWSLKDLPLAGAAVAASKTAADADIERVKLLLOVHASKQDISAEKQYKGIIDCYVR 60
DB 1 MTEQAISFAKDFELAGGIAAASIKTAADADIERVKLLLOVHASKQIAADAKQYKGIIDCYVR 60
QY 61 IPKRGFSLFMRGNANVIRFPPQALNFARFKDKYKQLFLGSDVDRHKQFMYRFPAGNLASG 120
DB 61 IPKRGVSLFMRGNANVIRFPPQALNFARFKDKYKQLFLGSDVDRHKQFMYRFPAGNLASG 120
QY 121 GAAGATSLCFYPLDFARTRIADVGR-AQREFHGLDGCIIKIPKSGDLGKVGQFNVS 179
DB 121 GAAGATSLCFYPLDFARTRIADVGR-AQREFHGLDGCIIKIPKSGDLGKVGQFNVS 179
QY 180 VOGIITVRAAFEGYVDTRAKMLPDKNVHIFVSWMAIASVTAVAGLSYPPDYRRMM 239
DB 180 VOGIITVRAAFEGYVDTRAKMLPDKNVHIFVSWMAIASVTAVAGLSYPPDYRRMM 239
QY 240 OSGRGADIMVTGYDCKRRTAKDEGAALFRKGANSNVLRLMGAFVLYLYDEIKKYV 297
DB 240 OSGRGADIMVTGYDCKRRTAKDEGAALFRKGANSNVLRLMGAFVLYLYDEIKKYV 297
QY 241 OSGRGADIMVTGYDCKRRTAKDEGAALFRKGANSNVLRLMGAFVLYLYDEIKKYV 298
DB 241 OSGRGADIMVTGYDCKRRTAKDEGAALFRKGANSNVLRLMGAFVLYLYDEIKKYV 298

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RESULT 9
ADT3_BOVIN STANDARD; PRT; 298 AA.
AC P32007;
DT 01-JUL-1993 (Rel. 26, Created)
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 16-OCT-2001 (Rel. 40, Last annotation update)
DE ADP/ATP carrier protein, isoform T2 (ADP/ATP translocase 3) (Adenine
  nucleotide translocator 3) (ANT 3).
GN SLC25A6 OR ANT3
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP MEDLINE-89229093; PubMed-2540808;
RX Powell S.J., Medd S.M., Runswick M.J., Walker J.E.;
RT "Two bovine genes for mitochondrial ADP/ATP translocase expressed
  differences in various tissues.";
RL Biochemistry 28:866-873(1989).
CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
CC MITOCHONDRIAL INNER MEMBRANE.
CC -1- SUBUNIT: Homodimer.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
  inner membrane.
CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
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  the European Bioinformatics Institute. There are no restrictions on its
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  entities requires a license agreement (See http://www.isb-sib.ch/announce/
  or send an email to license@isb-sib.ch).
CC -----
DR EMBL: M24103; AAA30769.1; -
DR PIR: B43646; B43646.
DR InterPro: IPR002067; Mlt_carrier.
DR InterPro: IPR002030; Mlt_uncoupling.
DR InterPro: IPR001993; Mlt_c_carrier.
DR Pfam: PF00153; Mlt_c_carrier_3.
DR PRINTS: PR00926; MITOCARRIER.
DR PRINTS: PR00784; MTUNCOUPLING.
DR PROSITE: PS00215; MITOCH_CARRIER_3.
KM Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
KW Multigene family.
FT TRANSMEM 12 29 1 (POTENTIAL).
FT TRANSMEM 73 91 2 (POTENTIAL).
FT TRANSMEM 117 134 3 (POTENTIAL).
FT TRANSMEM 176 195 4 (POTENTIAL).
FT TRANSMEM 214 231 5 (POTENTIAL).
FT TRANSMEM 273 291 6 (POTENTIAL).
FT REPEAT 2 111 1.
FT REPEAT 112 208 2.
FT REPEAT 209 298 3.
SQ SEQUENCE 298 AA; 32877 MW; 1C34E7DF6DE4061 CRC64;

Query Match 88.9%; Score 1380.5; DB 1; Length 298;
Best local Similarity 86.9%; Pred. No. 2.4e-116;
Matches 259; Conservative 21; Mismatches 17; Indels 1; Gaps 1;
QY 1 MGDHANSFLKDFLAGVAAAVSTAPAPLERVYKLLQVGHASQISAEQYKGIIDCVAR 60
DB 1 MTEQALISFKADFLAGGIAAISTAAPIERVKLLQVGHASQIADQYKGIIDCVAR 60
QY 1 IREKQGLSFWKGNLANVIRYPTQALNFAFKDKYKQLFGVDRHKQFWRYPAGMLASG 120
DB 61 IREKQGLSFWKGNLANVIRYPTQALNFAFKDKYKQLFGVDRHKQFWRYPAGMLASG 120
DB 61 IREKQGLSFWKGNLANVIRYPTQALNFAFKDKYKQLFGVDRHKQFWRYPAGMLASG 120

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RESULT 10
ADT_DROME STANDARD; PRT; 299 AA.
AC Q26365; P91614; Q26254; Q95S30; Q9VZ70;
DT 15-JUL-1998 (Rel. 36, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE ADP/ATP carrier protein (ADP/ATP translocase) (Adenine nucleotide
  translocator) (ANT) (Stress sensitive B protein).
GN SSB OR A/A-T OR C616944.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-92389367; PubMed-1387687;
RL Louvi A., Tellion S.G.;
RT "A cDNA clone encoding the ADP/ATP translocase of Drosophila
  melanogaster shows a high degree of similarity with the mammalian
  ADP/ATP translocases.";
RL J. Mol. Evol. 35:44-50(1992).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE-94350065; PubMed-7520869;
RL Hutter P., Karch F.;
RT "Molecular analysis of a candidate gene for the reproductive
  isolation between sibling species of Drosophila.";
RL Experientia 50:749-762(1994).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN-Oregon-R.
RA Zhang Y.Q., Davis A.W., Roote J., Herrmann S., Ashburner M.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN-Berkeley.
RX MEDLINE-20196006; PubMed-10731132;
RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
  Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
  George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
  Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
  Brandon R.C., Rogers Y.-H.C., Blazer R.G., Chame M., Pfeiffer B.D.,
  Wen K.H., Doyle C., Baxter E.G., Helt G., Neilson C.R., Milos G.L.G.,
  Abril J.F., Abmayyan A., An H.-J., Andrews-Frankoch C., Baldwin D.,
  Ballwey R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
  Beeson K.Y., Benos P.V., Bertan B.P., Bhandari D., Bolshakov S.,
  Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotlier P.,
  Burris R.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
  Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
  de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
  Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
  Durbin K.J., Evangelista C.C., Ferraz C., Ferrieres S., Fleischmann W.,
  Foster G., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
  Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
  Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
  Hostin D., Houston K.A., Howland T.J., Wei M.-H., Idegami C.,
  Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

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Db 1 MADAISFLKDFLAGVAAAIKSTAVAPIERVKLLLOVHASKOIAADKOKGIIDCYVR 60
QY 1PKEOGFLSFWRGNLANVIRYPTQALNFAFKDKYKOLFGVNRHKOFRYFAGNLASG 120
Db 61 IPKOGVLSFWRGNLANVIRYPTQALNFAFKDKYKOLFGVNRHKOFRYFAGNLASG 120
QY 121 GAAGATSLCFYYPDPFARTRLADYGR-AGREFHGLDCLIKIRKSDGLKLYOGFNVS 179
Db 121 GAAGATSLCFYYPDPFARTRLADYGR-AGREFHGLDCLIKIRKSDGLKLYOGFNVS 180
QY 180 VOGIITIRAAVFGYIDTAAGMLPDPKRNHIFVSMIAOSVAVAGLSTPFDYVRRMM 239
Db 181 VOGIITIRAAVFGYIDTAAGMLPDPKRNHIFVSMIAOSVAVAGLSTPFDYVRRMM 240
QY 240 QSGRKGADIMYTGIVDCWRKIAKDEGAKAFKGAWSNVLRGMGAFVLYLDEIKKYV 297
Db 241 QSGRKGADIMYTGIVDCWRKIAKDEGAKAFKGAWSNVLRGMGAFVLYLDEIKKYV 298

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RESULT 5

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QYIC4 PRELIMINARY: PRT: 298 AA.
AC 09YIC4:
DT 01-MAY-1999 (TREMBLrel. 10, Created)
DT 01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE ADP/ATP translocase.
OS Rana rugosa (Wrinkled frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
NC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
OX NCBI_TaxID=8410;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-99083429; PubMed-9866197;
RA Miura I., Ohtani H., Nakamura M., Ichikawa Y., Saitoh K.;
RT "The origin and differentiation of the heteromorphic sex chromosomes
RT z, w, x, and y in the frog Rana rugosa, inferred from the sequences of
RT a sex-linked gene, ADP/ATP translocase.";
RL Mol. Biol. Evol. 15:1612-1619(1998).
CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
DR EMBL; AB008463; BAA36513.1; -
DR InterPro: IPR001993; Mitoch_carrier.
DR InterPro: IPR002067; Mlt_carrier.
DR InterPro: IPR002030; Mlt_uncoupling.
DR Pfam: PF00153; mltc_carr; 3.
DR PRINTS: PR00926; MITOCARRIER.
DR PRINTS: PR00784; MTUNCOUPLING.
DR PROSITE: PS00215; MITOCH_CARRIER; 3.
KW Membrane; Transmembrane; Transport.
SQ SEQUENCE 298 AA; 33068 MW; 15B270ED37099A00 CRC64;

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Query Match 88.7%; Score 1377.5; DB 13; Length 298;
 Best Local Similarity 86.6%; Pred. No. 1e-120;
 Matches 258; Conservative 23; Mismatches 16; Indels 1; Gaps 1;

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QY 1 MGDHMSFLKDFLAGVAAAVSKTAVAPIERVKLLLOVHASKOISAEKOKGIIDCYVR 60
Db 1 MTDAAISPAKDFLAGVAAAIKSTAVAPIERVKLLLOVHASKOITADKOKYGINDCYVR 60
QY 61 IPKOGFLSFWRGNLANVIRYPTQALNFAFKDKYKOLFGVNRHKOFRYFAGNLASG 120
Db 61 IPKOGFLSFWRGNLANVIRYPTQALNFAFKDKYKOLFGVNRHKOFRYFAGNLASG 120
QY 121 GAAGATSLCFYYPDPFARTRLADYGR-AGREFHGLDCLIKIRKSDGLKLYOGFNVS 179
Db 121 GAAGATSLCFYYPDPFARTRLADYGR-AGREFHGLDCLIKIRKSDGLKLYOGFNVS 180
QY 180 VOGIITIRAAVFGYIDTAAGMLPDPKRNHIFVSMIAOSVAVAGLSTPFDYVRRMM 239
Db 181 VOGIITIRAAVFGYIDTAAGMLPDPKRNHIFVSMIAOSVAVAGLSTPFDYVRRMM 240
QY 240 QSGRKGADIMYTGIVDCWRKIAKDEGAKAFKGAWSNVLRGMGAFVLYLDEIKKYV 297

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Db 241 QSGRKGADIMYTGIVDCWRKIAKDEGAKAFKGAWSNVLRGMGAFVLYLDEIKKYI 298

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RESULT 6

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QYPRH1 PRELIMINARY: PRT: 298 AA.
AC 09PRH1:
DT 01-MAY-2000 (TREMBLrel. 13, Created)
DT 01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE ADP/ATP translocase.
OS Rana rugosa (Wrinkled frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
NC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Ranidae; Rana.
OX NCBI_TaxID=8410;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-99083429; PubMed-9866197;
RA Miura I., Ohtani H., Nakamura M., Ichikawa Y., Saitoh K.;
RT "The origin and differentiation of the heteromorphic sex chromosomes
RT z, w, x, and y in the frog Rana rugosa, inferred from the sequences of
RT a sex-linked gene, ADP/ATP translocase.";
RL Mol. Biol. Evol. 15:1612-1619(1998).
CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
DR EMBL; AB008463; BAA36513.1; -
DR EMBL; AB008456; BAA36506.1; -
DR EMBL; AB008461; BAA36511.1; -
DR EMBL; AB008462; BAA36512.1; -
DR InterPro: IPR001993; Mitoch_carrier.
DR InterPro: IPR002067; Mlt_carrier.
DR InterPro: IPR002030; Mlt_uncoupling.
DR Pfam: PF00153; mltc_carr; 3.
DR PRINTS: PR00926; MITOCARRIER.
DR PRINTS: PR00784; MTUNCOUPLING.
DR PROSITE: PS00215; MITOCH_CARRIER; 3.
KW Membrane; Transmembrane; Transport.
SQ SEQUENCE 298 AA; 33054 MW; B0E23AD56F548D36 CRC64;

```

Query Match 88.7%; Score 1377.5; DB 13; Length 298;
 Best Local Similarity 86.6%; Pred. No. 1e-120;
 Matches 258; Conservative 23; Mismatches 16; Indels 1; Gaps 1;

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QY 1 MGDHMSFLKDFLAGVAAAVSKTAVAPIERVKLLLOVHASKOISAEKOKGIIDCYVR 60
Db 1 MTDAAISPAKDFLAGVAAAIKSTAVAPIERVKLLLOVHASKOITADKOKYGINDCYVR 60
QY 61 IPKOGFLSFWRGNLANVIRYPTQALNFAFKDKYKOLFGVNRHKOFRYFAGNLASG 120
Db 61 IPKOGFLSFWRGNLANVIRYPTQALNFAFKDKYKOLFGVNRHKOFRYFAGNLASG 120
QY 121 GAAGATSLCFYYPDPFARTRLADYGR-AGREFHGLDCLIKIRKSDGLKLYOGFNVS 179
Db 121 GAAGATSLCFYYPDPFARTRLADYGR-AGREFHGLDCLIKIRKSDGLKLYOGFNVS 180
QY 180 VOGIITIRAAVFGYIDTAAGMLPDPKRNHIFVSMIAOSVAVAGLSTPFDYVRRMM 239
Db 181 VOGIITIRAAVFGYIDTAAGMLPDPKRNHIFVSMIAOSVAVAGLSTPFDYVRRMM 240
QY 240 QSGRKGADIMYTGIVDCWRKIAKDEGAKAFKGAWSNVLRGMGAFVLYLDEIKKYV 297
Db 241 QSGRKGADIMYTGIVDCWRKIAKDEGAKAFKGAWSNVLRGMGAFVLYLDEIKKYI 298

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DB 1 MTDAAISAKDFLAGVAAASKTAVALPIERVKLLQVOHASKQITADKHKIGIMDCYVR 60
OY 61 IPKEDGSLFWRGNLANVIRYPTQALNFAFKDKYKQFLGVDNRHKOFRYFAGNLASG 120
DB 61 IPKEDGSLFWRGNLANVIRYPTQALNFAFKDKYKQFLGVDNRHKOFRYFAGNLASG 120
OY 121 GAAGATSLCFYVPLDFARTRLADYVGRRA-QREFHGLDCCIIFKSDGLKGLYOGFNVS 179
DB 121 GAAGATSLCFYVPLDFARTRLADYVGRRA-QREFHGLDCCIIFKSDGLKGLYOGFNVS 180
OY 180 VOGIITRAAYFGYIDTAAGMLPDPKNTPIFVSMIAQVTAAGFASYPEDTVRRMM 239
DB 181 VOGIITRAAYFGYIDTAAGMLPDPKNTPIFVSMIAQVTAAGFASYPEDTVRRMM 240
OY 240 QSGRGADIMYTGVDCKRIAKDEGAKAFKFGANSVLRGKGAFVLYLDEIKKYV 297
DB 241 QSGRGADIMYTGVDCKRIAKDEGAKAFKFGANSVLRGKGAFVLYLDEIKKYV 298

RESULT 10
OY 095VX4 PRELIMINARY; PRT; 299 AA.
AC 095VX4:
DT 01-DEC-2001 (Tremblrel. 19, Created)
DT 01-DEC-2001 (Tremblrel. 19, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE ADP-ATP translocase.
OS Ethmostigmus rubripes.
OC Eukaryota; Metazoa; Arthropoda; Myriapoda; Chilopoda;
OC Pleurostilmophora; Scolopendromorpha; Scolopendridae; Ethmostigmus.
OX NCBI_TaxID=62613;
RN [1]
RA Burnell J.N.;
RT "Nucleotide sequence of an ADP-ATP translocator of Ethmostigmus
RT rubripes."
RL Submitted (JUL-2001) to the EMBL/Genbank/DBJ databases.
DR EMBL; AF401758; AAL02100.1;
DR InterPro; IPR001993; Mitoch_carrier.
DR Pfam; PF00153; mito_carrier.
DR PRINTS; PR00926; MITOCARRIER.
DR PROSITE; PS00215; MITOCH_CARRIER; 3.
SQ SEQUENCE 299 AA; 33037 MW; 3C3B0CB26E7C3C5E CRC64;

Query Match 80.2%; Score 1245.5; DB 5; Length 299;
Best Local Similarity 80.3%; Pred. No. 2.3e-108;
Matches 236; Conservative 25; Mismatches 32; Indels 1; Gaps 1;

OY 5 AWSFLKDFLAGVAAAVASKTAVAPIERVKLLQVOHASKQISAEKQYKGIIDCVRIKPE 64
DB 5 AWSFLKDFLAGVAAAVASKTAVAPIERVKLLQVOHASKQISAEKQYKGIIDCVRIKPE 64
OY 65 OGSFLFWRGNLANVIRYPTQALNFAFKDKYKQFLGVDNRHKOFRYFAGNLASGAG 124
DB 65 OGSFLFWRGNLANVIRYPTQALNFAFKDKYKQFLGVDNRHKOFRYFAGNLASGAG 124
OY 125 ATSLCFYVPLDFARTRLADYVGR-RAQREFHGLDCCIIFKSDGLKGLYOGFNVSOCI 183
DB 125 ATSLCFYVPLDFARTRLADYVGR-RAQREFHGLDCCIIFKSDGLKGLYOGFNVSOCI 184
OY 184 IIRAAAYGVYDTAKGMLPDPKNTPIFVSMIAQVTAAGFASYPEDTVRRMMQSGR 243
DB 185 IIRAAAYGVYDTAKGMLPDPKNTPIFVSMIAQVTAAGFASYPEDTVRRMMQSGR 244
OY 244 KGADIMYTGVDCKRIAKDEGAKAFKFGANSVLRGKGAFVLYLDEIKKYV 297
DB 245 KGADIMYTGVDCKRIAKDEGAKAFKFGANSVLRGKGAFVLYLDEIKKYV 298

RESULT 11
OY 09NHWS PRELIMINARY; PRT; 300 AA.
ID 09NHWS

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AC 09NHWS;
DT 01-OCT-2000 (Tremblrel. 15, Created)
DT 01-OCT-2000 (Tremblrel. 15, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE ADP-ATP translocase.
OS Lucilia cuprina (greenbottle fly) (Australian sheep blowfly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
OX Calliphoridae; Lucilia.
OX NCBI_TaxID=7375;
RN [1]
RA SEQUENCE FROM N.A.
RC STRAIN=SS mal seeking;
RA Chen Z., Fair J.A., Batterham P.;
RT "A DNA clone encoding the ADP/ATP translocase of Lucilia cuprina."
RL Submitted (DEC-1999) to the EMBL/Genbank/DBJ databases.
CC -1 SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
DR EMBL; AF218587; AAF32322.1;
DR InterPro; IPR001993; Mitoch_carrier.
DR Pfam; PF00153; mito_carrier.
DR PRINTS; PR00926; MITOCARRIER.
DR PROSITE; PS00215; MITOCH_CARRIER; 3.
KW Membrane; Transmembrane; Transport.
SQ SEQUENCE 300 AA; 33036 MW; 5459DF0EAD0E2E742 CRC64;

Query Match 79.9%; Score 1241.5; DB 5; Length 300;
Best Local Similarity 78.7%; Pred. No. 5.6e-108;
Matches 236; Conservative 25; Mismatches 36; Indels 3; Gaps 1;

OY 1 MGDHA---WSFLKDFLAGVAAAVASKTAVAPIERVKLLQVOHASKQISAEKQYKGIIDC 57
DB 1 MGDHAADPLGFYKDFEAGISAAVSKTAVAPIERVKLLQVOHISKQISPDQYKGMIDC 60
OY 58 VRIKEDGSLFWRGNLANVIRYPTQALNFAFKDKYKQFLGVDNRHKOFRYFAGNL 117
DB 61 FVRIKEDGSLFWRGNLANVIRYPTQALNFAFKDKYKQFLGVDNRHKOFRYFAGNL 120
OY 118 ASGGAAGATSLCFYVPLDFARTRLADYVGRRAQREFHGLDCCIIFKSDGLKGLYOGFN 177
DB 121 ASGGAAGATSLCFYVPLDFARTRLADYVGRRAQREFHGLDCCIIFKSDGLKGLYOGFN 180
OY 178 VSVGGIITRAAYFGYIDTAAGMLPDPKNTPIFVSMIAQVTAAGFASYPEDTVRRMM 237
DB 181 VSVGGIITRAAYFGYIDTAAGMLPDPKNTPIFVSMIAQVTAAGFASYPEDTVRRMM 240
OY 238 MMQSGRGADIMYTGVDCKRIAKDEGAKAFKFGANSVLRGKGAFVLYLDEIKKYV 297
DB 241 MMQSGRGADIMYTGVDCKRIAKDEGAKAFKFGANSVLRGKGAFVLYLDEIKKYV 300

RESULT 12
OY 08IRA0 PRELIMINARY; PRT; 312 AA.
ID 08IRA0
AC 08IRA0;
DT 01-MAR-2003 (Tremblrel. 23, Created)
DT 01-MAR-2003 (Tremblrel. 23, Last sequence update)
DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
DE CG16944-PC.
GN SE8B.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OX Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RA SEQUENCE FROM N.A.
RC MEDLINE=20196006; PubMed=10731132;
RA Adams M.D., Cealiker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galie R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Mortan J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.H., Blazek R.G., Champagne M., Pfeiffer B.D.,

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RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gabor G.L.,
 RA April J.F., Agbayan A., An H.J., Andrews-Pfannkuch C., Baldwin D.,
 RA Ballew R.M., Baau A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Besson P.V., Berman B.P., Bhandari P., Bolshakov S.,
 RA Borkova D., Botchan M.R., Bouck J., Brakstein D., Brotler P.,
 RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cavley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Domes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Foster C., Gabriellian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Idegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lin Z.,
 RA Laske P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Mishina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacleb J.M.,
 RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spletter E., Spreading A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.Y., Wasserman D.A., Weinstock G.M., Weissbach J.,
 RA Williams S.M., Woodrager, Morley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
 RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,
 RA "The genome sequence of Drosophila melanogaster."

[2]
 RP SEQUENCE FROM N.A.
 RA Centliker S.E., Adams M.D., Krommiller B., Wan K.H., Holt R.A.,
 RA Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,
 RA Banton J., An H., Baldwin D., Banton J., Beeson K.Y., Busam D.A.,
 RA Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
 RA Dodson K., Dorssett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,
 RA Ferreira S., Frisze E., Galle R.F., Garg N.S., George R.A.,
 RA Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
 RA Idegwam C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,
 RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,
 RA Pacleb J., Paragas V., Park S., Patel S., Pfeiffer B.,
 RA Phoumenavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,
 RA Stapleton M., Strong R., Svirskas R., Tector C., Tyler D.,
 RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.,
 RA "Sequencing of Drosophila melanogaster genome."
 RT Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

[3]
 RP SEQUENCE FROM N.A.
 RA Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
 RA Hradecky P., Huang Y., Kaminker J.S., Prochuk S.E., Smith C.D.,
 RA Tupy J.L., Bergman C., Berman B., Carlson J.W., Centliker S.E.,
 RA Clump M., Drysdale R., Emmert D., Frisze E., de Grey A., Harris N.,
 RA Krommiller B., Marshall B., Millburn G., Richter J., Russo S.,
 RA Seearle S.M.J., Smith E., Shu S., Smutniak F., Whitfield E.,
 RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.,
 RA "Annotation of Drosophila melanogaster genome."
 RT Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

[4]
 RP SEQUENCE FROM N.A.
 RA Adams M.D., Centliker S.E., Gibbs R.A., Rubin G.M., Venter C.J.,
 RA Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.

[5]
 RP SEQUENCE FROM N.A.

RA FlyBase;
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AEO03484; AAN09267.1; -
 SO SEQUENCE 312 AA; 34214 MW; 70D5634E74E168DF CRC64;

Query Match 79.9%; Score 1241; DB 5; Length 312;

Best Local Similarity 79.7%; Pred. No. 6,66-108;
 Matches 232; Conservative 26; Mismatches 33; Indels 0; Gaps 0;
 QY 5 AMSFLKQFLGAVAAVAAVSKTAVAPTRVRLKLLQVQHSKOISAKOYKGIIDCVRRPK 64
 DB 20 AVGFVKDFPAAGGISAASKTAVAPTRVRLKLLQVQHSKOISAKOYKGIIDCVRRPK 79
 QY 65 QGFLSPFRGNLANVIRFPQALNFAFKDKYKQFLGCVDRHKKQFWRYFAGNLASGAAG 124
 DB 80 QGFSFPRGNLANVIRFPQALNFAFKDKYKQFLGCVDRHKKQFWRYFAGNLASGAAG 139
 QY 125 ATSCFYPPLDFANTRLAADYGRARQREPHGLGCCIIRKISDGLRGLYGFNVSGCII 184
 DB 140 ATSCFYPPLDFANTRLAADYGRARQREPHGLGCCIIRKISDGLRGLYGFNVSGCII 199
 QY 185 IYRAAYGVDTAGMPPDPKNVIFVSMIAQSVTVAGLSYEPFTVRRMMQSGRK 244
 DB 200 IYRAAYGVDTAGMPPDPKNVIFVSMIAQSVTVAGLSYEPFTVRRMMQSGRK 259
 QY 245 GADIMYGTVDQWKRKAKDEGAKAFKGAANSVLRGGAFFVLVLYDEIRK 295
 DB 260 ATEVIYKNTLHCWATIKQEGTGAFFKGAANSVLRGGAFFVLVLYDEIRK 310

RESULT 13
 ID Q91336 PRELIMINARY; PRT; 317 AA.
 AC Q91336;
 DT 01-NOV-1996 (TREMURel. 01, Created)
 DT 01-MAY-1999 (TREMURel. 10, Last sequence update)
 DT 01-MAR-2003 (TREMURel. 23, Last annotation update)
 DE ADP/ATP translocase.
 OS Rana sylvatica (Wood Frog).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranoidae; Rana.
 CX NCBI_TaxID=45438;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver.
 RX MEDLINE=97398141; PubMed=9256066;
 RA Cal O., Greenway S.C., Storey K.B.;
 RT "Differential regulation of the mitochondrial ADP/ATP translocase gene
 RL in wood frogs under freezing stress."
 RN Blochum. Biophys. Acta 1353:69-78(1997).
 [2]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver.
 RA Cal O., Storey K.B.;
 RL Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
 DR EMBL: U44832; AAA97882.2; -
 DR InterPro: IPR001993; Mitoch carrier.
 DR InterPro: IPR002067; Mit. carrier.
 DR Pfam: PF00153; mito_carr; 3.
 DR PRINTS: PRO0926; MITOCHARRIER.
 DR PROSITE: PS00215; MITOCH_CARRIER. 3.
 KW Membrane; Transmembrane; Transport.
 SO SEQUENCE 317 AA; 35005 MW; 5F66B7ED8D5CEB72 CRC64;

Query Match 79.5%; Score 1234.5; DB 13; Length 317;
 Best Local Similarity 85.7%; Pred. No. 2,7e-107;
 Matches 233; Conservative 21; Mismatches 17; Indels 1; Gaps 1;

QY 1 MGDHAWFLDPLAGAAVAAVSKTAVAPTRVRLKLLQVQHSKOISAKOYKGIIDCVRR 60
 DB 1 MTDANSFADPLAGAAVAAVSKTAVAPTRVRLKLLQVQHSKOISAKOYKGIIDCVRR 60
 QY 61 IPKEQGLSPFRGNLANVIRFPQALNFAFKDKYKQFLGCVDRHKKQFWRYFAGNLASG 120
 DB 61 IPKEQGLSPFRGNLANVIRFPQALNFAFKDKYKQFLGCVDRHKKQFWRYFAGNLASG 120
 QY 121 GAAGATSLCFVYPLDFANTRLAADYGRARQREPHGLGCCIIRKISDGLRGLYGFNV 179
 DB 121 GAAGATSLCFVYPLDFANTRLAADYGRARQREPHGLGCCIIRKISDGLRGLYGFNV 179


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DB 121 GAAGATSLCFVYPLDFAKRLADYKAGAGREFNGLADCLAKIFKSDGLKGLYOGFNVS 180
QY 180 VGGIIIRAAVFGYDTAKGMLPDPKRVHIFVSMIAQSYAVAGILSPEDYVRRMM 239
DB 181 VGGIIIRAAVFGYDTAKGMLPDPKRVHIFVSMIAQSYAVAGILSPEDYVRRMM 240
QY 240 QSGRKGADIMYTGVDCKRIAKDEGAKAFPK 271
DB 241 QSGRKGAEIMYSGTIDCKRIARDEGGRAPFR 272

RESULT 14
O44094 PRELIMINARY; PRT; 288 AA.
AC O44094;
DT 01-JUN-1998 (TREMblrel. 06, Created)
DT 01-JUN-1998 (TREMblrel. 06, last sequence update)
DT 01-MAR-2003 (TREMblrel. 23, last annotation update)
DE ADP/ATP translocase (Fragment).
GN SESB.
OS Drosophila subobscura (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OK NCBI_TaxID=7241;
RN [1]
RP SEQUENCE FROM N.A.
RA Zeng L.-W., Comeron J.M., Chen B., Kreitman M.;
RL Genetics 0:0-0(1997).
CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
DR EMBL; AF025799; AAB87884.1; -.
DR Flybase; FBgn0023237; Dsub\sesb.
DR InterPro; IPR001993; Mitoch_carrier.
DR InterPro; IPR002067; Mlt_carrier.
DR Pfam; PF00153; mltc_carr; 3.
DR PRINTS; PR00926; MITOCARRIER.
DR PROSITE; PS00215; MITOCH_CARRIER; 3.
KW Membrane; Repeat; Transmembrane; Transport.
FT NON_TER 288
SQ SEQUENCE 288 AA; 31775 MW; 06A1D1E477E81B26 CRC64;

Query Match 76.2%; Score 1183; DB 5; Length 288;
Best Local Similarity 79.6%; Pred. No. 1.6e-102;
Matches 226; Conservative 23; Mismatches 33; Indels 2; Gaps 2;

QY 5 AMSFLKDFLAGVANAASKTAVAPIERVKLLQVQHASKQISAERQYGIIDCVIRIKE 64
DB 7 AIGFVKDFPAGGISAASKTAVAPIERVKLLQVQHASKQISAERQYGIIDCVIRIKE 66
QY 65 QGFLSFWRGNLANVIRYFPTQALNFAFKDKYKQLFLGVDVRRHKOFWRYPFAGNLASGAAG 124
DB 67 QGFSSEFWRGNLANVIRYFPTQALNFAFKDKYKQYFLGVDKNTQFWRYPFAGNLASGAAG 126
QY 125 ATSLCFVYPLDFAKRLADYKAGAGREFNGLADCLAKIFKSDGLKGLYOGFNVSQGIT 184
DB 127 ATSLCFVYPLDFAKRLADYKAGAGREFNGLADCLAKIFKSDGLKGLYOGFNVSQGIT 186
QY 185 IYRAAYFGYDTAKGMLPDPKRVHIFVSMIAQSYAVAGILSPEDYVRRMMQSGRK 244
DB 187 IYRAAYFGYDTAKGMLPDPKRVHIFVSMIAQSYAVAGILSPEDYVRRMMQSGRK 245
QY 245 GADIMYTGVDCKRIAKDEGAKAFPKGAMSNVNLGMSGAFVLY 288
DB 246 ATEIIYKNTLHGMATIAQEGS-AFFKGAFSNVNLGMSGAFVLY 288

RESULT 15
O44093 PRELIMINARY; PRT; 288 AA.
AC O44093;
DT 01-JUN-1998 (TREMblrel. 06, Created)
DT 01-JUN-1998 (TREMblrel. 06, last sequence update)
DT 01-MAR-2003 (TREMblrel. 23, last annotation update)

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DE ADP/ATP translocase (Fragment).
GN SESB.
OS Drosophila pseudoobscura (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OK NCBI_TaxID=7237;
RN [1]
RP SEQUENCE FROM N.A.
RA Zeng L.-W., Comeron J.M., Chen B., Kreitman M.;
RL Genetics 0:0-0(1997).
CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
DR EMBL; AF025798; AAB87883.1; -.
DR Flybase; FBgn0023292; Dpse\sesb.
DR InterPro; IPR001993; Mitoch_carrier.
DR InterPro; IPR002067; Mlt_carrier.
DR Pfam; PF00153; mltc_carr; 3.
DR PRINTS; PR00926; MITOCARRIER.
DR PROSITE; PS00215; MITOCH_CARRIER; 3.
KW Membrane; Repeat; Transmembrane; Transport.
FT NON_TER 288
SQ SEQUENCE 288 AA; 31725 MW; 052B0CC0050436B0 CRC64;

Query Match 76.2%; Score 1183; DB 5; Length 288;
Best Local Similarity 79.6%; Pred. No. 1.6e-102;
Matches 226; Conservative 25; Mismatches 31; Indels 2; Gaps 2;

QY 5 AMSFLKDFLAGVANAASKTAVAPIERVKLLQVQHASKQISAERQYGIIDCVIRIKE 64
DB 7 AIGFVKDFPAGGISAASKTAVAPIERVKLLQVQHASKQISAERQYGIIDCVIRIKE 66
QY 65 QGFLSFWRGNLANVIRYFPTQALNFAFKDKYKQLFLGVDVRRHKOFWRYPFAGNLASGAAG 124
DB 67 QGFSSEFWRGNLANVIRYFPTQALNFAFKDKYKQYFLGVDKNTQFWRYPFAGNLASGAAG 126
QY 125 ATSLCFVYPLDFAKRLADYKAGAGREFNGLADCLAKIFKSDGLKGLYOGFNVSQGIT 184
DB 127 ATSLCFVYPLDFAKRLADYKAGAGREFNGLADCLAKIFKSDGLKGLYOGFNVSQGIT 186
QY 185 IYRAAYFGYDTAKGMLPDPKRVHIFVSMIAQSYAVAGILSPEDYVRRMMQSGRK 244
DB 187 IYRAAYFGYDTAKGMLPDPKRVHIFVSMIAQSYAVAGILSPEDYVRRMMQSGRK 245
QY 245 GADIMYTGVDCKRIAKDEGAKAFPKGAMSNVNLGMSGAFVLY 288
DB 246 ATEIIYKNTLHGMATIAQEGS-AFFKGAFSNVNLGMSGAFVLY 288

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Search completed: August 28, 2003, 19:42:09
Job time : 53.2206 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 28, 2003, 19:27:31 ; Search time 52.3919 Seconds
(without alignments)
902.821 Million cell updates/sec

Title: US-09-811-132-32

Perfect score: 1547
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Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1107863 seqs, 158726573 residues

Total number of hits satisfying chosen parameters: 1107863

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

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25: /SIDSL/gcgdata/geneseq/geneseqp-emb1/AA2003.DAT.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Length | DB ID | Description |
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| 1 | 1547 | 100.0 | 298 21 | AAV71032 Human adenine nucl |
| 2 | 1547 | 100.0 | 298 22 | AAU01037 Human adenine nucl |
| 3 | 1547 | 100.0 | 298 23 | AAU01037 Human adenine nucl |
| 4 | 1537 | 100.0 | 298 23 | AAO18516 Human insulin rece |
| 5 | 1454 | 94.0 | 298 21 | AAV71033 Human adenine nucl |
| 6 | 1454 | 94.0 | 22 | AAK39641 Human polypeptide |
| 7 | 1454 | 94.0 | 298 22 | AAU01200 Human adenine nucl |
| 8 | 1454 | 94.0 | 298 23 | AAU01038 Human adenine nucl |
| 9 | 1454 | 94.0 | 323 22 | AAW41427 Human polypeptide |

| | | | | | | |
|----|--------|------|------|----|----------|--------------------|
| 10 | 1417 | 91.6 | 325 | 22 | ABG15423 | Novel human diagno |
| 11 | 1411 | 91.2 | 298 | 19 | AAW61169 | Anti protein. Mus |
| 12 | 1409 | 91.1 | 293 | 22 | ABU53219 | Human metabolism-a |
| 13 | 1391.5 | 89.9 | 297 | 21 | AAV71031 | Human adenine nucl |
| 14 | 1391.5 | 89.9 | 297 | 22 | AAU01198 | Human adenine nucl |
| 15 | 1391.5 | 89.9 | 297 | 23 | AAU01037 | Human adenine nucl |
| 16 | 1346 | 87.0 | 263 | 22 | ABG27056 | Novel human diagno |
| 17 | 1339 | 86.6 | 429 | 24 | ABR41715 | Human DTRP organe |
| 18 | 1253.5 | 81.0 | 299 | 22 | ABB66082 | Drosophila melanog |
| 19 | 1253.5 | 81.0 | 299 | 22 | ABB67300 | Drosophila melanog |
| 20 | 1125.5 | 72.8 | 307 | 22 | ABB56380 | Drosophila melanog |
| 21 | 1102 | 71.2 | 315 | 22 | ABU53218 | Human metabolism-a |
| 22 | 1102 | 71.2 | 315 | 23 | AAE21175 | Human TRICH-19 pro |
| 23 | 988 | 63.9 | 228 | 23 | ABP43205 | Human ovarian anti |
| 24 | 923 | 59.7 | 222 | 23 | ABP74106 | Human TRICH SEQ ID |
| 25 | 895.5 | 57.9 | 298 | 22 | ABG18922 | Novel human diagno |
| 26 | 792 | 51.2 | 484 | 22 | ABG15422 | Novel human diagno |
| 27 | 792 | 51.2 | 484 | 22 | ABG27055 | Novel human diagno |
| 28 | 779.5 | 50.4 | 301 | 23 | ABP73357 | Candida albicans e |
| 29 | 747.5 | 48.3 | 346 | 21 | AAG36577 | Arabidopsis thalia |
| 30 | 747.5 | 48.3 | 346 | 21 | AAG37261 | Arabidopsis thalia |
| 31 | 747.5 | 48.3 | 346 | 21 | AAG37264 | Arabidopsis thalia |
| 32 | 747.5 | 48.3 | 346 | 21 | AAG38460 | Arabidopsis thalia |
| 33 | 747.5 | 48.3 | 363 | 21 | AAG36576 | Arabidopsis thalia |
| 34 | 747.5 | 48.3 | 363 | 21 | AAG37260 | Arabidopsis thalia |
| 35 | 747.5 | 48.3 | 363 | 21 | AAG37263 | Arabidopsis thalia |
| 36 | 747.5 | 48.3 | 363 | 21 | AAG38459 | Arabidopsis thalia |
| 37 | 747.5 | 48.3 | 381 | 21 | AAG36575 | Arabidopsis thalia |
| 38 | 747.5 | 48.3 | 381 | 21 | AAG37259 | Arabidopsis thalia |
| 39 | 747.5 | 48.3 | 381 | 21 | AAG37262 | Arabidopsis thalia |
| 40 | 747.5 | 48.3 | 381 | 21 | AAG38458 | Arabidopsis thalia |
| 41 | 747.5 | 48.3 | 992 | 21 | AAG38672 | Arabidopsis thalia |
| 42 | 747.5 | 48.3 | 1009 | 21 | AAG38671 | Arabidopsis thalia |
| 43 | 747.5 | 48.3 | 1027 | 21 | AAG38670 | Arabidopsis thalia |
| 44 | 746 | 48.2 | 379 | 24 | ABP81267 | Arabidopsis thalia |
| 45 | 744.5 | 48.1 | 346 | 21 | AAG17731 | Arabidopsis thalia |

ALIGNMENTS

| | | |
|----------|--|-------------------------------------|
| RESULT 1 | AAV71032 | AAV71032 standard; Protein; 298 AA. |
| ID | AAV71032 | AAV71032 standard; Protein; 298 AA. |
| XX | AAV71032 | AAV71032 standard; Protein; 298 AA. |
| AC | AAV71032 | AAV71032 standard; Protein; 298 AA. |
| XX | AAV71032 | AAV71032 standard; Protein; 298 AA. |
| DT | 29-AUG-2000 | (first entry) |
| XX | 29-AUG-2000 | (first entry) |
| DE | Human adenine nucleotide translocator ANT2. | |
| XX | Human adenine nucleotide translocator ANT2. | |
| XX | Human adenine nucleotide translocator ANT2. | |
| KW | Human: adenine nucleotide translocator; ANT2; mitochondria; ADP; ATP; adenosine triphosphate; adenosine triphosphate; apoptosis; MPT; cancer; mitochondrial permeability transition; neuroprotective; neuroleptic; antiparkinsonian; cytosolic; antidiabetic; anticonvulsant; neuroleptic; antiparkinsonian; cytosolic; antidiabetic; anticonvulsant; neuroleptic; Alzheimer's disease; Parkinson's disease; Huntington's disease; dysontia; diabetes; leber's hereditary optic neuropathy; schizophrenia; MELAS; mitochondrial encephalopathy; lactic acidosis; stroke; MIDD; mitochondrial diabetes and deafness; hyperproliferative disorder; myoclonic epilepsy red ragged fibre syndrome. | |
| KW | Human: adenine nucleotide translocator; ANT2; mitochondria; ADP; ATP; adenosine triphosphate; adenosine triphosphate; apoptosis; MPT; cancer; mitochondrial permeability transition; neuroprotective; neuroleptic; antiparkinsonian; cytosolic; antidiabetic; anticonvulsant; neuroleptic; antiparkinsonian; cytosolic; antidiabetic; anticonvulsant; neuroleptic; Alzheimer's disease; Parkinson's disease; Huntington's disease; dysontia; diabetes; leber's hereditary optic neuropathy; schizophrenia; MELAS; mitochondrial encephalopathy; lactic acidosis; stroke; MIDD; mitochondrial diabetes and deafness; hyperproliferative disorder; myoclonic epilepsy red ragged fibre syndrome. | |
| KW | Human: adenine nucleotide translocator; ANT2; mitochondria; ADP; ATP; adenosine triphosphate; adenosine triphosphate; apoptosis; MPT; cancer; mitochondrial permeability transition; neuroprotective; neuroleptic; antiparkinsonian; cytosolic; antidiabetic; anticonvulsant; neuroleptic; antiparkinsonian; cytosolic; antidiabetic; anticonvulsant; neuroleptic; Alzheimer's disease; Parkinson's disease; Huntington's disease; dysontia; diabetes; leber's hereditary optic neuropathy; schizophrenia; MELAS; mitochondrial encephalopathy; lactic acidosis; stroke; MIDD; mitochondrial diabetes and deafness; hyperproliferative disorder; myoclonic epilepsy red ragged fibre syndrome. | |
| OS | Homo sapiens. | |
| XX | Homo sapiens. | |
| XX | Homo sapiens. | |
| PN | WO200026370-A2. | |
| XX | WO200026370-A2. | |
| PD | 11-MAY-2000. | |
| XX | 11-MAY-2000. | |
| PF | 03-NOV-1999; | 99WO-US25883. |
| XX | 03-NOV-1999; | 99WO-US25883. |
| PR | 03-NOV-1998; | 98US-0185904. |
| XX | 03-NOV-1998; | 98US-0185904. |
| XX | 08-SEP-1999; | 99US-0393441. |
| XX | 08-SEP-1999; | 99US-0393441. |

PA (MITO-) MITOKOR.
 XX
 PI Anderson CM, Davis RE, Clevenger W, Wiley SE, Miller SW, Szabo TR;
 PI Ghosh SS;
 XX
 DR WPI: 2000-365619/31.
 DR N-PSDB; AAD00520.
 XX
 PT Recombinant construct encoding adenine nucleotide translocator
 PT polypeptide, useful e.g. in screening for potential therapeutic agents
 PT against mitochondrial disease -
 XX
 PS Claim 45; Page 172-173; 175pp; English.
 XX
 CC The patent discloses a method to produce adenine nucleotide translocator
 CC (ANT) proteins or ANT fusion proteins using recombinant expression
 CC constructs. ANT is a nuclear encoded protein and a major component of
 CC inner mitochondrial membrane. It mediates transport of adenosine
 CC di/tri-phosphates across the mitochondrial inner membrane and also serves
 CC as an important molecular component of the mitochondrial permeability
 CC transition pore, a modulator of apoptosis. ANT is used to identify agents
 CC or ligands that bind to, or interact with it. The ANT ligands are used to
 CC detect or isolate ANT in a biological sample, and therapeutically for
 CC regulating mitochondrial pore activity, for treating diseases associated
 CC with altered mitochondrial function, including Alzheimer's, Parkinson's
 CC and Huntington's diseases, cancer, psoriasis, diabetes, dystonia,
 CC Leber's hereditary optic neuropathy, schizophrenia, mitochondrial
 CC encephalopathy, lactic acidosis and stroke (MELAS), hyperproliferative
 CC disorders, mitochondrial diabetes and deafness (MID), and myoclonic
 CC epilepsy red ragged fibre syndrome. The present sequence is an
 CC adenine nucleotide translocator ANT2 from human brain.
 CC
 XX
 SQ Sequence 298 AA;
 Query Match 100.0%; Score 1547; DB 21; Length 298;
 Best Local Similarity 100.0%; Pred. No. 2,3e-154;
 Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MTDALSPAKDFLAGVAAIAISKTAAPIERVKLLQOVHASKQITADKQKGIIDCVR 60
 DB 1 MTDALSPAKDFLAGVAAIAISKTAAPIERVKLLQOVHASKQITADKQKGIIDCVR 60
 QY 61 IPKEQVLSFWNRGNLANVIRYPTQALNFAFKDKYQIFLGVDKRTQFRRYAGNLIASG 120
 DB 61 IPKEQVLSFWNRGNLANVIRYPTQALNFAFKDKYQIFLGVDKRTQFRRYAGNLIASG 120
 QY 121 GAAGATSLCFVYPLDFARTRILADVGKAGAREFERGLGDCLVYIKSDGKIGLYOGFNVS 180
 DB 121 GAAGATSLCFVYPLDFARTRILADVGKAGAREFERGLGDCLVYIKSDGKIGLYOGFNVS 180
 QY 181 VOGIITIRAAVREGIYDTAKGMLPDPKNTHTIVISMIAQVTAAGLTSPFDVRRRMM 240
 DB 181 VOGIITIRAAVREGIYDTAKGMLPDPKNTHTIVISMIAQVTAAGLTSPFDVRRRMM 240
 QY 241 QSGRKGTIDIMYGTLLDCWKRIADDEGKAFKAGMSNVLRGMGAVLVLYIDEIKKYYT 298
 DB 241 QSGRKGTIDIMYGTLLDCWKRIADDEGKAFKAGMSNVLRGMGAVLVLYIDEIKKYYT 298
 RESULT 2
 AAU01199
 ID AAU01199 standard; Protein; 298 AA.
 XX
 AC AAU01199;
 XX
 DT 07-SEP-2001 (first entry)
 XX
 DE Human adenine nucleotide translocator-2 (ANT-2) protein.
 KW Human; adenine nucleotide translocator-2; ANT-2; MTP; cyclophilin;
 KW mitochondrial permeability transition pore component; cell survival;
 KW mitochondrial core component; mitochondrial related disorder; cancer;
 KW Alzheimer's disease; diabetes mellitus; hyperproliferative disorder.

XX
 OS Homo sapiens.
 XX
 PN WO200132876-A2.
 XX
 PD 10-MAY-2001.
 XX
 PF 03-NOV-2000; 2000WO-US30535.
 XX
 PR 03-NOV-1999; 99US-0434354.
 XX
 PA (MITO-) MITOKOR.
 XX
 PI Murphy AN, Clevenger W, Wiley SE, Andreyev AY, Frigeri LG;
 PI Velicelcib G, Davis RE;
 XX
 DR WPI: 2001-291054/30.
 DR N-PSDB; AAS05902.
 XX
 PT New nucleic acid expression constructs, useful for screening for agents
 PT that alter mitochondrial permeability transition (MPT), comprises
 PT polynucleotide encoding MPT polypeptide or cyclophilin polypeptide
 PT fused to energy transfer molecule -
 XX
 PS Disclosure; Fig 2; 186pp; English.
 XX
 CC The present sequence represents human adenine nucleotide translocator-2
 CC (ANT-2) protein. ANT proteins are mitochondrial permeability
 CC transition (MPT) pore components responsible for mediating transport
 CC of ADP across the mitochondrial inner membrane. ANT proteins interact
 CC with other mitochondrial core components e.g. cyclophilins to
 CC regulate MPT. The present invention relates to a novel nucleic acid
 CC expression construct comprising a promoter operably linked to a
 CC polynucleotide encoding a mitochondrial pore component polypeptide
 CC (e.g. ANT) fused to an energy transfer molecule (ETM) protein
 CC (e.g. green fluorescent protein (GFP) or a FLASH sequence). The novel
 CC expression construct can alter mitochondrial membrane permeability
 CC transition and/or alter the interaction between mitochondrial core
 CC components. The methods are useful for screening for agents that alter
 CC MPT and/or cell survival. These agents are useful for the prevention or
 CC treatment of diseases associated with altered mitochondrial function or
 CC dysfunctional cell survival, such as Alzheimer's disease, diabetes
 CC mellitus, Parkinson's disease, Huntington's disease, schizophrenia,
 CC mitochondrial encephalopathy, lactic acidosis, stroke,
 CC hyperproliferative disorders e.g. cancer, and deafness.
 CC
 XX
 SQ Sequence 298 AA;
 Query Match 100.0%; Score 1547; DB 22; Length 298;
 Best Local Similarity 100.0%; Pred. No. 2,3e-154;
 Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MTDALSPAKDFLAGVAAIAISKTAAPIERVKLLQOVHASKQITADKQKGIIDCVR 60
 DB 1 MTDALSPAKDFLAGVAAIAISKTAAPIERVKLLQOVHASKQITADKQKGIIDCVR 60
 QY 61 IPKEQVLSFWNRGNLANVIRYPTQALNFAFKDKYQIFLGVDKRTQFRRYAGNLIASG 120
 DB 61 IPKEQVLSFWNRGNLANVIRYPTQALNFAFKDKYQIFLGVDKRTQFRRYAGNLIASG 120
 QY 121 GAAGATSLCFVYPLDFARTRILADVGKAGAREFERGLGDCLVYIKSDGKIGLYOGFNVS 180
 DB 121 GAAGATSLCFVYPLDFARTRILADVGKAGAREFERGLGDCLVYIKSDGKIGLYOGFNVS 180
 QY 181 VOGIITIRAAVREGIYDTAKGMLPDPKNTHTIVISMIAQVTAAGLTSPFDVRRRMM 240
 DB 181 VOGIITIRAAVREGIYDTAKGMLPDPKNTHTIVISMIAQVTAAGLTSPFDVRRRMM 240
 QY 241 QSGRKGTIDIMYGTLLDCWKRIADDEGKAFKAGMSNVLRGMGAVLVLYIDEIKKYYT 298
 DB 241 QSGRKGTIDIMYGTLLDCWKRIADDEGKAFKAGMSNVLRGMGAVLVLYIDEIKKYYT 298

RESULT 3
AA010379
ID AA010379 standard; Protein; 298 AA.
XX
XX
AA010379;
AC
XX
XX
14-FEB-2002 (first entry)
DT
XX
XX
Human adenine nucleotide translocator 2 (ANT2).
DE
XX
XX
Human; adenine nucleotide translocator; ANT; ss;
KM
XX
XX
mitochondrial matrix protein.
KW
XX
XX
Homo sapiens.
OS
XX
XX
WO200185944-A2.
PN
XX
XX
15-NOV-2001.
PD
XX
XX
11-MAY-2001; 2001WO-US15416.
PF
XX
XX
11-MAY-2000; 2000US-0569327.
PR
XX
XX
11-MAY-2000; 2000US-0569327.
PS
XX
XX
(MITO-) MITOKOR.
PA
XX
XX
Anderson CM, Davis RE, Clevenger W, Willey SE, Miller SM, Szabo TR;
PI
XX
XX
Ghosh SS, Moos WH, Pel Y, Carroll AK;
DR
XX
XX
MPI: 2002-055598/07.
N-PSDB; AAS16689.
DR
XX
XX
Novel recombinant expression construct for producing adenine nucleotide
PT
XX
XX
translocator polypeptides, comprises a regulated promoter linked to
PT
XX
XX
nucleic acid encoding the polypeptide -
PS
XX
XX
Claim 44; Fig 2; 147pp; English.
PS
XX
XX
The invention relates to a recombinant expression construct (I)
CC
XX
XX
comprising a regulated promoter operably linked to a nucleic acid
CC
XX
XX
encoding an adenine nucleotide translocator (ANT) polypeptide. ANT
CC
XX
XX
proteins mediate the exchange of ATP synthesised in the mitochondrial
CC
XX
XX
matrix for ADP in the cytosol. (I) is useful for producing recombinant
CC
XX
XX
ANT polypeptide by transforming a prokaryotic or eukaryotic host cell and
CC
XX
XX
culturing the host cell. (I) is also useful for targeting a polypeptide
CC
XX
XX
of interest to a mitochondrial membrane, where ANT polypeptide is
CC
XX
XX
expressed as a fusion protein with the polypeptide of interest.
CC
XX
XX
Recombinant ANT polypeptide, or cells expressing the polypeptide, is
CC
XX
XX
useful for identifying an agent that binds to an ANT polypeptide. ANT
CC
XX
XX
ligand is useful for determining the presence of an ANT polypeptide,
CC
XX
XX
preferably ANT1, ANT2 or ANT3 in a biological sample and for isolating
CC
XX
XX
ANT from a biological sample, where the ANT ligand is covalently or non-
CC
XX
XX
covalently bound to a solid phase. Detectably labeled ANT ligand is also
CC
XX
XX
useful for identifying an agent that interacts with an ANT polypeptide.
CC
XX
XX
The present sequence represents the amino acid sequence of human ANT2.
SQ
Sequence 298 AA;

Query Match 100.0%; Score 1547; DB 23; Length 298;
Best Local Similarity 100.0%; Pred. No. 2.3e-154;
Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY 1 MTDAALSPAKDFLAGVAAAIKSTAVAPIERVKLLQVYHASKQITADKQYGIIDCVYR 60
DB 1 MTDAALSPAKDFLAGVAAAIKSTAVAPIERVKLLQVYHASKQITADKQYGIIDCVYR 60
OY 61 IKREDEVISFWMGANLANVIRYPTQALNFAFDKDKYQIIFLGVDKFTQFWRFPAGMLASG 120
DB 61 IKREDEVISFWMGANLANVIRYPTQALNFAFDKDKYQIIFLGVDKFTQFWRFPAGMLASG 120
OY 121 GAAGTSLCFEYVPLDFARTRLADYKAGAREFRGSGCIYKITYSDGKIGYGFNVS 180
DB 121 GAAGTSLCFEYVPLDFARTRLADYKAGAREFRGSGCIYKITYSDGKIGYGFNVS 180

OY 181 VGGIIIRAAVFGIYDPFAGKMLPDPKNTHTHVISMMAQFVAVAGLTSPFDTVRRRMM 240
DB 181 VGGIIIRAAVFGIYDPFAGKMLPDPKNTHTHVISMMAQFVAVAGLTSPFDTVRRRMM 240
OY 241 QSGRKGTDMYTGTLDCKRRIARDEGKAFFKAGMSNVLRGSGAFVLYLYDEIKRYT 298
DB 241 QSGRKGTDMYTGTLDCKRRIARDEGKAFFKAGMSNVLRGSGAFVLYLYDEIKRYT 298
RESULT 4
AA018516
ID AA018516 standard; Protein; 298 AA.
XX
XX
AA018516;
AC
XX
XX
11-OCT-2002 (first entry)
DT
XX
XX
Human insulin receptor signaling modifier SEQ ID NO: 54.
DE
XX
XX
Human; insulin receptor signaling; insulin receptor signaling modifier;
KM
XX
XX
ISM; diabetes; metabolic syndrome; antidiabetic.
OS
XX
XX
Homo sapiens.
PN
XX
XX
WO200255664-A2.
PD
XX
XX
18-JUL-2002.
PF
XX
XX
11-JAN-2002; 2002WO-US01048.
PR
XX
XX
12-JAN-2001; 2001US-261226P.
PR
XX
XX
12-JAN-2001; 2001US-261303P.
PR
XX
XX
12-JAN-2001; 2001US-261304P.
PR
XX
XX
12-JAN-2001; 2001US-261335P.
PR
XX
XX
12-JAN-2001; 2001US-261336P.
PR
XX
XX
12-JAN-2001; 2001US-261361P.
PR
XX
XX
12-JAN-2001; 2001US-261456P.
PR
XX
XX
12-JAN-2001; 2001US-261457P.
PR
XX
XX
12-JAN-2001; 2001US-261458P.
PR
XX
XX
12-JAN-2001; 2001US-261459P.
PR
XX
XX
12-JAN-2001; 2001US-261461P.
PR
XX
XX
12-JAN-2001; 2001US-261518P.
PR
XX
XX
12-JAN-2001; 2001US-261531P.
PR
XX
XX
12-JAN-2001; 2001US-261532P.
PR
XX
XX
12-JAN-2001; 2001US-261589P.
PR
XX
XX
12-JAN-2001; 2001US-261590P.
PR
XX
XX
12-JAN-2001; 2001US-261649P.
PR
XX
XX
12-JAN-2001; 2001US-261656P.
PR
XX
XX
12-JAN-2001; 2001US-261697P.
PA
XX
XX
(EXEL-) EXELIXIS INC.
PI
XX
XX
Seidel-Dugan C, Ferguson KC, Kidd T;
DR
XX
XX
N-PSDB; AAL48635.
DR
XX
XX
MPI: 2002-599664/64.
PT
XX
XX
Identifying an insulin receptor signaling modulator, useful as drug
PT
XX
XX
targets for treating diabetes or metabolic disorders, comprises
PT
XX
XX
contacting an assay system comprising insulin receptor signaling
PT
XX
XX
modifiers with a test agent -
PS
XX
XX
Disclosure: Page 160-161; 232pp; English.
PS
XX
XX
The present invention relates to a method of identifying a candidate
CC
XX
XX
insulin receptor (INR) signaling modulating agent, involving contacting
CC
XX
XX
an assay system comprising an insulin receptor signaling modifier (ISM)
CC
XX
XX
polypeptide or nucleic acid with a test agent, and detecting a test
CC
XX
XX
agent-biased activity of the assay system. The method is useful for
CC
XX
XX
identifying candidate INR signaling modulating agents. ISM genes may be
CC
XX
XX
used as drug targets for treatment of disorders related to INR signaling
CC
XX
XX
such as diabetes or metabolic syndrome. ISM nucleic acids and
CC
XX
XX
polypeptides are useful for identifying and testing agents that modulate

CC ISM function and for other applications related to the involvement of ISM
CC in INR signaling, and for identifying subjects having a predisposition to
CC such diseases associated with INR signaling. The present sequence is an
CC ISM protein described in the exemplification of the invention.

SO Sequence 298 AA;

Query Match 99.4%; Score 1537; DB 23; Length 298;
Best Local Similarity 99.3%; Pred. No. 2,6e-153;
Matches 296; Conservative 1; Mismatches 1; Indels 0; Gaps 0;

QY 1 MTDAALSFANDFLAGVAAAIKSTAAVAPIERVKLLLOVHAASKQITADKQKGIIDCVR 60
DB 1 MTDAALSFANDFLAGVAAAIKSTAAVAPIERVKLLLOVHAASKQITADKQKGIIDCVR 60
QY 61 IPKEQVLSFMRGNLANVIRFPTQALNFAEKDKYKQIFLGVDVKRTQFMRFFAGNLSG 120
DB 61 IPKEQVLSFMRGNLANVIRFPTQALNFAEKDKYKQIFLGVDVKRTQFMRFFAGNLSG 120
QY 121 GAAGATSLCFVYPLDFARTRLADVGKAGAREFERGLGDCLVKTKSDGKIGLYQGFNVS 180
DB 121 GAAGATSLCFVYPLDFARTRLADVGKAGAREFERGLGDCLVKTKSDGKIGLYQGFNVS 180
QY 121 VGGITIRAAVFGIYDPAKGLPDPKNTHTVISMIAQTYAVAGLTSYPTDVRRRMM 240
DB 181 VGGITIRAAVFGIYDPAKGLPDPKNTHTVISMIAQTYAVAGLTSYPTDVRRRMM 240
QY 241 QSGRKGTDIMYTGTLDCKRKIARDEGKAFKFGAMS NVLKGMGAFVLYLYDEIKRYT 298
DB 241 QSGRKGTDIMYTGTLDCKRKIARDEGKAFKFGAMS NVLKGMGAFVLYLYDEIKRYT 298

RESULT 5

AAV71033 standard; Protein: 298 AA.

AC AAV71033;
DT 29-AUG-2000 (first entry)
DE Human adenine nucleotide translocator ANT3.

XX Human; adenine nucleotide translocator; ANT3; mitochondria; ADP; ATP;
KW adenosine diphosphate; adenosine tri-phosphate; apoptosis; MPT; cancer;
KW mitochondrial permeability transition; neuroprotective; nocitropic;
KW antiParkinsonian; cytosolic; antidiabetic; anticonvulsant; neuroleptic;
KW antiparkinsonian; cytosolic; antidiabetic; anticonvulsant; neuroleptic;
KW Alzheimer's disease; Parkinson's disease; Huntington's disease; dystonia;
KW diabetes; leber's hereditary optic neuropathy; schizophrenia; MELAS;
KW mitochondrial encephalopathy; lactic acidosis; stroke; MIDD;
KW mitochondrial diabetes and deafness; hyperproliferative disorder;
KW myoclonic epilepsy red ragged fibre syndrome.

XX Homo sapiens.
PN WO200026370-A2.

PD 11-MAY-2000.

PF 03-NOV-1999; 99WO-US25883.

PR 03-NOV-1998; 98US-0185904.

PR 08-SEP-1999; 99US-0393441.

PA (MITO-) MITOKOR.

PI Anderson CM, Davis RE, Clevenger W, Wiley SE, Miller SM, Szabo TR;
PI Ghosh SS;

XX MPI; 2000-365619/31.

XX N-PSDB; AAD00521.
XX Recombinant construct encoding adenine nucleotide translocator
PT

PT polypeptide, useful e.g. in screening for potential therapeutic agents
PT against mitochondrial disease
PS Claim 46; Page 173-174; 175pp; English.

CC The patent discloses a method to produce adenine nucleotide translocator
CC (ANT) proteins or ANT fusion proteins using recombinant expression
CC constructs. ANT is a nuclear encoded protein and a major component of
CC inner mitochondrial membrane. It mediates transport of adenosine
CC diphosphate across the mitochondrial inner membrane and also serves
CC as an important molecular component of the mitochondrial permeability
CC transition pore, a modulator of apoptosis. ANT is used to identify agents
CC or ligands that bind to, or interact with it. The ANT ligands are used to
CC detect or isolate ANT in a biological sample, and therapeutically for
CC regulating mitochondrial pore activity, for treating diseases associated
CC with altered mitochondrial function, including Alzheimer's, Parkinson's
CC and Huntington's diseases, cancer, psoriasis, diabetes, dystonia,
CC leber's hereditary optic neuropathy, schizophrenia, mitochondrial
CC encephalopathy, lactic acidosis and stroke (MELAS), hyperproliferative
CC disorders, mitochondrial diabetes and deafness (MIDD), and myoclonic
CC epilepsy red ragged fibre syndrome. The present sequence is an
CC adenine nucleotide translocator ANT3 from human brain.

XX Sequence 298 AA;

Query Match 94.0%; Score 1454; DB 21; Length 298;
Best Local Similarity 92.6%; Pred. No. 1.4e-144;
Matches 274; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

QY 1 MTDAALSFANDFLAGVAAAIKSTAAVAPIERVKLLLOVHAASKQITADKQKGIIDCVR 60
DB 1 MTEQALISFANDFLAGVAAAIKSTAAVAPIERVKLLLOVHAASKQITADKQKGIIDCVR 60
QY 61 IPKEQVLSFMRGNLANVIRFPTQALNFAEKDKYKQIFLGVDVKRTQFMRFFAGNLSG 120
DB 61 IPKEQVLSFMRGNLANVIRFPTQALNFAEKDKYKQIFLGVDVKRTQFMRFFAGNLSG 120
QY 121 GAAGATSLCFVYPLDFARTRLADVGKAGAREFERGLGDCLVKTKSDGKIGLYQGFNVS 180
DB 121 GAAGATSLCFVYPLDFARTRLADVGKAGAREFERGLGDCLVKTKSDGKIGLYQGFNVS 180
QY 121 VGGITIRAAVFGIYDPAKGLPDPKNTHTVISMIAQTYAVAGLTSYPTDVRRRMM 240
DB 181 VGGITIRAAVFGIYDPAKGLPDPKNTHTVISMIAQTYAVAGLTSYPTDVRRRMM 240
QY 181 VGGITIRAAVFGIYDPAKGLPDPKNTHTVISMIAQTYAVAGLTSYPTDVRRRMM 240
DB 181 VGGITIRAAVFGIYDPAKGLPDPKNTHTVISMIAQTYAVAGLTSYPTDVRRRMM 240
QY 241 QSGRKGTDIMYTGTLDCKRKIARDEGKAFKFGAMS NVLKGMGAFVLYLYDEIKRYT 296
DB 241 QSGRKGTDIMYTGTLDCKRKIARDEGKAFKFGAMS NVLKGMGAFVLYLYDEIKRYT 296

RESULT 6

AAV39641 standard; Protein: 298 AA.

AC AAV39641;

DT 22-OCT-2001 (first entry)

DE Human polypeptide SEQ ID NO 2786.

XX Human; neurotrophic; immunosuppressant; cytosolic; gene therapy; cancer;
KW peripheral nervous system; neuropathy; central nervous system; CNS;
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW chemokine; thrombolytic; drug screening; arthritis; inflammation;
KW leukaemia.

XX Homo sapiens.

XX WO200153312-A1.

XX 26-JUL-2001.
XX

PF 26-DEC-2000; 2000MO-US34263.
 XX
 XX 21-JAN-2000; 2000US-0488725.
 PR 25-APR-2000; 2000US-0552317.
 PR 09-JUL-2000; 2000US-0598042.
 PR 19-JUL-2000; 2000US-0620312.
 PR 03-AUG-2000; 2000US-0653450.
 PR 14-SEP-2000; 2000US-0662191.
 PR 19-OCT-2000; 2000US-0693036.
 PR 29-NOV-2000; 2000US-0727344.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
 PI Wang J, Wang Z, Weinman T, Xu C, Xue AJ, Yang Y, Zhang J;
 PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;
 XX
 DR WPI: 2001-442253/47.
 DR N-PSDB: AA158797.
 XX
 PT Novel nucleic acids and polypeptides, useful for treating disorders
 PT such as central nervous system injuries -
 XX
 PS Example 4: SEQ ID NO 2786; 10078bp; English.
 XX
 CC The invention relates to human nucleic acids (AA157798-AA161369) and
 CC the encoded polypeptides (AAM38642-AAM42213) with nootropic,
 CC immunosuppressant and cytoskeletal activity. The polynucleotides are useful
 CC in gene therapy. A composition containing a polypeptide or polynucleotide
 CC of the invention may be used to treat diseases of the peripheral nervous
 CC system, such as peripheral nervous injuries, peripheral neuropathy and
 CC localized neuropathies and central nervous system diseases, such as
 CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
 CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
 CC utilisation of the activities such as: Immune system suppression,
 CC Activin/inhibin activity, chemotactic/chemokinetic activity, haemostatic
 CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
 CC assays for receptor activity, arthritis and inflammation, leukaemias and
 CC C.N.S disorders.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification.
 CC
 XX Sequence 298 AA:
 SQ
 Query Match 94.0%; Score 1454; DB 22; Length 298;
 Best Local Similarity 92.6%; Pred. No. 1.4e-144;
 Matches 274; Conservative 13; Mismatches 9; Indels 0; Gaps 0;
 QY 1 MTDALSFAPKDFLAGVAAIAISTAVAPIERVKLLQOVHASKQITADKQYKGIIDCVVR 60
 DB 1 MTEQAISFAPKDFLAGGIAAIAISTAVAPIERVKLLQOVHASKQIADKQYKGIIDCVVR 60
 QY 1 PREQEVLSFWRNGLANVIRYPTQALNFAFKDKYKQIFLGVDKRTQFRYRAGNLASG 120
 DB 61 IREQGVLSFWRNGLANVIRYPTQALNFAFKDKYKQIFLGVDKRTQFRYRAGNLASG 120
 QY 121 GAAGATSLCFVYPLDFARTRLADYKAGAREFRGIDGLVYIKYSDGIRGLYOGFNSV 180
 DB 121 GAAGATSLCFVYPLDFARTRLADYKAGAREFRGIDGLVYIKYSDGIRGLYOGFNSV 180
 QY 181 VGGIITTYRAAYGITYTAKGMLPDPKNTHTIVISWMAQOYTVAVAGLTSTPFDTVRRRMM 240
 DB 181 VGGIITTYRAAYGITYTAKGMLPDPKNTHTIVISWMAQOYTVAVAGVSYFPDVRRRMM 240
 QY 241 OSGRKGTDMYGTGLDLCMKRIADDEGKAFKFGAMSNVIRMGAGCAVLYYDEIKK 296
 DB 241 OSGRKGTDMYGTGLDLCMKRIADDEGKAFKFGAMSNVIRMGAGCAVLYYDEIKK 296
 RESULT 7
 AAU01200
 ID AAU01200 standard; Protein; 298 AA.

AC AAU01200;
 XX
 XX 07-SEP-2001 (first entry)
 DE Human adenine nucleotide translocator-3 (ANT-3) protein.
 XX
 XX Human: adenine nucleotide translocator-3; ANT-3; MPT; cyclophilin;
 KW mitochondrial permeability transition pore component; cell survival;
 KW mitochondrial core component; mitochondrial related disorder; cancer;
 KW Alzheimer's disease; diabetes mellitus; hyperproliferative disorder.
 XX
 OS Homo sapiens.
 XX
 PN WO200132876-A2.
 XX
 PD 10-MAY-2001.
 XX
 PF 03-NOV-2000; 2000MO-US30535.
 XX
 PR 03-NOV-1999; 99US-0434354.
 XX
 PA (MITO-) MITOKOR.
 XX
 PI Murphy AN, Cleveenger W, Willey SE, Andreyev AY, Frliger LG;
 PI Velicelebi G, Davis RE;
 XX
 DR WPI: 2001-291054/30.
 DR N-PSDB: AAS05903.
 XX
 PT New nucleic acid expression constructs, useful for screening for agents
 PT that alter mitochondrial permeability transition (MPT), comprises
 PT polynucleotide encoding MPT polypeptide or cyclophilin polypeptide
 PT fused to energy transfer molecule -
 XX
 PS Disclosure; Fig 2; 186bp; English.
 XX
 CC The present sequence represents human adenine nucleotide translocator-3
 CC (ANT-3) protein. ANT proteins are mitochondrial permeability
 CC transition (MPT) pore components responsible for mediating transport
 CC of ADP across the mitochondrial inner membrane. ANT proteins interact
 CC with other mitochondrial core components e.g. cyclophilins to
 CC regulate MPT. The present invention relates to a novel nucleic acid
 CC expression construct comprising a promoter operably linked to a
 CC polynucleotide encoding a mitochondrial pore component polypeptide
 CC (e.g. ANT) fused to an energy transfer molecule (ETM) protein
 CC (e.g. green fluorescent protein (GFP) or a FLASH sequence). The novel
 CC expression construct can alter mitochondrial membrane permeability
 CC transition and/or alter the interaction between mitochondrial core
 CC components. The methods are useful for screening for agents that alter
 CC MPT and/or cell survival. These agents are useful for the prevention or
 CC treatment of diseases associated with altered mitochondrial function or
 CC dysfunctional cell survival, such as Alzheimer's disease, diabetes
 CC mellitus, Parkinson's disease, Huntington's disease, schizophrenia,
 CC mitochondrial encephalopathy, lactic acidosis, stroke,
 CC hyperproliferative disorders e.g. cancer, and deafness.
 CC
 XX Sequence 298 AA:
 SQ
 Query Match 94.0%; Score 1454; DB 22; Length 298;
 Best Local Similarity 92.6%; Pred. No. 1.4e-144;
 Matches 274; Conservative 13; Mismatches 9; Indels 0; Gaps 0;
 QY 1 MTDALSFAPKDFLAGVAAIAISTAVAPIERVKLLQOVHASKQITADKQYKGIIDCVVR 60
 DB 1 MTEQAISFAPKDFLAGGIAAIAISTAVAPIERVKLLQOVHASKQIADKQYKGIIDCVVR 60
 QY 1 PREQEVLSFWRNGLANVIRYPTQALNFAFKDKYKQIFLGVDKRTQFRYRAGNLASG 120
 DB 61 IREQGVLSFWRNGLANVIRYPTQALNFAFKDKYKQIFLGVDKRTQFRYRAGNLASG 120
 QY 121 GAAGATSLCFVYPLDFARTRLADYKAGAREFRGIDGLVYIKYSDGIRGLYOGFNSV 180
 DB 121 GAAGATSLCFVYPLDFARTRLADYKAGAREFRGIDGLVYIKYSDGIRGLYOGFNSV 180

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OY 181 VGGIIITRAAFEGLYDTRAKGMLPDPKNTHTIVISMIAQVTAVAGLSYPEDTVRRMM 240
DB 181 VGGIIITRAAFEGYDTRAKGMLPDPKNTHTIVISMIAQVTAVAGVSYPEDTVRRMM 240
OY 241 QSGRRGADIMTYGTGLDCMRKRTARDEGKAPFKGAMSNVLRMGAFVLVLYDELK 296
DB 241 QSGRRGADIMTYGTGLDCMRKRTARDEGKAPFKGAMSNVLRMGAFVLVLYDELK 296

RESULT 8
AAU10380
ID AAU10380 standard; Protein: 298 AA.
AC AAU10380;
DE 14-FEB-2002 (first entry)
XX Human adenine nucleotide translocator 3 (ANT3).
XX Human; adenine nucleotide translocator; ANT;
XX mitochondrial matrix protein.
XX Homo sapiens.
XX MO200185944-A2.
XX 15-NOV-2001.
XX 11-MAY-2001; 2001WO-US15416.
XX 11-MAY-2000; 2000US-0569327.
XX (MITO-) MITOKOR.
XX Anderson CM, Davis RE, Cleverger W, Wiley SE, Miller SM, Szabo TR;
XX Ghosh SS, Moos WH, Pei Y, Carroll AK;
XX N-PSDB; AAS16690.
XX WPI: 2002-055598/07.
XX Novel recombinant expression construct for producing adenine nucleotide
XX translocator polypeptides, comprises a regulated promoter linked to
XX nucleic acid encoding the polypeptide
XX Example 3; Fig 2; 147pp; English.
XX The invention relates to a recombinant expression construct (I)
XX comprising a regulated promoter operably linked to a nucleic acid
XX encoding an adenine nucleotide translocator (ANT) polypeptide. ANT
XX proteins mediate the exchange of ATP synthesised in the mitochondrial
XX matrix for ADP in the cytosol. (I) is useful for producing recombinant
XX ANT polypeptide by transforming a prokaryotic or eukaryotic host cell and
XX culturing the host cell. (I) is also useful for targeting a polypeptide
XX of interest to a mitochondrial membrane, where ANT polypeptide is
XX expressed as a fusion protein with the polypeptide of interest.
XX Recombinant ANT polypeptide, or cells expressing the polypeptide, is
XX useful for identifying an agent that binds to an ANT polypeptide. ANT
XX ligand is useful for determining the presence of an ANT polypeptide,
XX preferably ANT1, ANT2 or ANT3 in a biological sample and for isolating
XX ANT from a biological sample, where the ANT ligand is covalently or non-
XX covalently bound to a solid phase. Detectably labeled ANT ligand is also
XX useful for identifying an agent that interacts with an ANT polypeptide.
XX The present sequence represents the amino acid sequence of human ANT3.
XX
SQ Sequence 298 AA;
Query Match 94.0%; Score 1454; DB 23; Length 298;
Best Local Similarity 92.6%; Pred. No. 1.4e-144;
Matches 274; Conservative 13; Mismatches 9; Indels 0; Gaps 0;
OY 1 MTEAALSFADFLAGVAAAIKTAAPVIERVKLLLOVNASQITADKQYKGIIDCV 60
II: I:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:

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DB 1 MTEQALISFADFLAGGIAAIAIKTAAPVIERVKLLLOVNASQIAADKQYKGIIDCV 60
OY 61 IPKEQVLESEFRGNLANVIRFPTQALNFAFKDKYKQIFLGVDYKRTQFMRFGANLASG 120
DB 61 IPKEQVLESEFRGNLANVIRFPTQALNFAFKDKYKQIFLGVDYKRTQFMRFGANLASG 120
OY 121 GAAGATSLCEFYPLDFARTRLAADVGRKAGAREFERGLDCLVTKYSKGIGLYQGFNS 180
DB 121 GAAGATSLCEFYPLDFARTRLAADVGRKAGAREFERGLDCLVTKYSKGIGLYQGFNS 180
OY 181 VGGIIITRAAFEGYDTRAKGMLPDPKNTHTIVISMIAQVTAVAGVSYPEDTVRRMM 240
DB 181 VGGIIITRAAFEGYDTRAKGMLPDPKNTHTIVISMIAQVTAVAGVSYPEDTVRRMM 240
OY 241 QSGRRGADIMTYGTGLDCMRKRTARDEGKAPFKGAMSNVLRMGAFVLVLYDELK 296
DB 241 QSGRRGADIMTYGTGLDCMRKRTARDEGKAPFKGAMSNVLRMGAFVLVLYDELK 296

RESULT 9
AAM41427
ID AAM41427 standard; Protein: 323 AA.
AC AAM41427;
DE 22-OCT-2001 (first entry)
XX Human polypeptide SEQ ID NO 6358.
XX Human; nocotropic; immunosuppressant; cytostatic; gene therapy; cancer;
XX peripheral nervous system; neuropathy; central nervous system; CNS;
XX Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
XX amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
XX chemokine; thrombolytic; drug screening; arthritis; inflammation;
XX leukaemia.
XX Homo sapiens.
XX MO200153312-A1.
XX 26-JUL-2001.
XX 26-DEC-2000; 2000WO-US34263.
XX 21-JAN-2000; 2000US-0488725.
XX 25-APR-2000; 2000US-0552317.
XX 09-JUL-2000; 2000US-0598042.
XX 19-JUL-2000; 2000US-0620312.
XX 03-AUG-2000; 2000US-0653450.
XX 14-SEP-2000; 2000US-0662191.
XX 19-OCT-2000; 2000US-0693036.
XX 29-NOV-2000; 2000US-0727344.
XX (HSE-) HYSEQ INC.
XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
XX Wang J, Wang Z, Wehrman T, Xu C, Xue AD, Yang Y, Zhang J;
XX Zhao QA, Zhou P, Goodrich R, Drmanac RT;
XX WPI: 2001-442253/47.
XX N-PSDB; AAI60583.
XX Novel nucleic acids and polypeptides, useful for treating disorders
XX such as central nervous system injuries
XX Example 2; SEQ ID NO 6358; 10078pp; English.
XX The invention relates to human nucleic acids (AA157798-AA161369) and
XX the encoded polypeptides (AAM38642-AAM42213) with nocotropic,
XX immunosuppressant and cytostatic activity. The polynucleotides are useful
XX in gene therapy. A composition containing a polypeptide or polynucleotide
XX of the invention may be used to treat diseases of the peripheral nervous
XX system, such as peripheral nervous injuries, peripheral neuropathy and

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| | | |
|----|---|--|
| | CC | localised neuropathies and central nervous system diseases, such as |
| | CC | Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic |
| | CC | lateral sclerosis, and Shy-Drager Syndrome. Other uses include the |
| | CC | utilisation of the activities such as: Immune system suppression, |
| | CC | Activin/inhibin activity, chemotactic/chemokine activity, haemostatic |
| | CC | and thrombolytic activity, cancer diagnosis and therapy, drug screening, |
| | CC | assays for receptor activity, arthritis and inflammation, leukaemia and |
| | CC | C.N.S disorders. |
| | CC | Note: The sequence data for this patent did not form part of the printed |
| | CC | specification. |
| | XX | |
| | XX | |
| SQ | Sequence | 323 AA; |
| | Query Match | 94.0% Score 1454; DB 22; Length 323; |
| | Best Local Similarity | 92.6%, Pred. No. 1,6e-144; |
| | Matches 274; | Conservative 13; Mismatches 9; Indels 0; Gaps 0; |
| QY | 1 | MTEDAALSFANDEFLAGVNAALSTKAVAPIEHWKLLOVQHASKOTADKOYKGIIIDCYVR 60 |
| Dd | 26 | MTEBAISFANDFLGGLGIAAISTKVAPIERVKLLLOVHASKOIAADKOKIGIYDCIVR 85 |
| QY | 61 | IPKEBVLSPWGRNLNAVIRYPPTQALNFAFKDKKYQLFLGVDRKTOFWRYFAGNLASG 120 |
| Dd | 86 | IPKEQVLSFWRGNLANVIRFPPTQALNFAFKDKKYQLFLGVDRKHQTFWRFAGNLASG 145 |
| QY | 121 | GAAATSLCFYRPIDFARTRLAADVGKAAGERERBGDDCLVKKYSDGIGLYOGFNYS 180 |
| Dd | 146 | GAAATSLCFYRPIDFARTRLAADVGKSGTEREFGLDCLVKKYSDGIRGLYOGFSYS 205 |
| QY | 181 | VGGIITRAAFVFGIYDPAKGM.LPPEKNHIYISMILACTVAVNVGLTSYPTPTRRMM 240 |
| Dd | 206 | VGGIITRAAFVFGIYDPAKGM.LPPEKNHIYISMILACTVAVNVGLTSYPTPTRRMM 265 |
| QY | 241 | QSGRKGYDIMVTGTLDCKMR.IARDEGGAFFPKGAMSNVLRMGAFVLYLVEIKR 296 |
| Dd | 266 | QSGRKGYDIMVTGTLDCKMR.KIFRDGGGAFFPKGAMSNVLRMGAFVLYLVEIKR 321 |
| | RESULT 10 | |
| | ABGI5423 | |
| ID | ABGI5423 standard; Protein; 325 AA. | |
| XX | | |
| AC | ABGI5423; | |
| XX | | |
| DT | 18-FEB-2002 (first entry) | |
| XX | | |
| DE | Novel human diagnostic protein #15414. | |
| KW | Human; chromosome mapping; gene mapping; gene therapy; forensic; | |
| KM | food supplement; medical imaging; diagnostic; genetic disorder. | |
| XX | | |
| OS | Homo sapiens. | |
| XX | | |
| PN | WO200175067-A2. | |
| XX | | |
| PD | 11-OCT-2001. | |
| XX | | |
| PF | 30-MAR-2001; 2001WO-US08631. | |
| PR | 31-MAR-2000; 2000US-0540217. | |
| PR | 23-AUG-2000; 2000US-0649167. | |
| XX | | |
| PA | (HYSE-) HYSEQ INC. | |
| XX | | |
| PI | Drmanc RT, Liu C, Tang YT; | |
| XX | | |
| DR | WI; 2001-639362/73. | |
| XX | N-PADB; AAS79610. | |
| XX | | |
| PT | New isolated polynucleotide and encoded polypeptides, useful in | |
| PT | diagnostics, forensics, gene mapping, identification of mutations | |
| PT | responsible for genetic disorders or other traits and to assess | |
| PT | biodiversity - | |

| | |
|---------------------------|---|
| PS | Claim 20; SEQ ID NO 45782; 103pp; English. |
| XX | The invention relates to isolated polynucleotide (I) and |
| CC | polypeptide (II) sequences. (I) is useful as hybridisation probes, |
| CC | polymerase chain reaction (PCR) primers, oligomers, and for chromosome |
| CC | and gene mapping, and in recombinant production of (II). The |
| CC | polynucleotides are also used in diagnostics as expressed sequence tags |
| CC | for identifying expressed genes. (I) is useful in gene therapy techniques |
| CC | to restore normal activity of (II) or to treat disease states involving |
| CC | (II). (II) is useful for generating antibodies against it, detecting or |
| CC | quantitating a polypeptide in tissue, as molecular weight markers and as |
| CC | a food supplement. (II) and its binding partners are useful in medical |
| CC | imaging of sites expressing (II). (I) and (II) are useful for treating |
| CC | disorders involving aberrant protein expression or biological activity. |
| CC | The polypeptide and polynucleotide sequences have applications in |
| CC | diagnostics, forensics, gene mapping, identification of mutations |
| CC | responsible for genetic disorders or other traits to assess biodiversity |
| CC | and to produce other types of data and products dependent on DNA and |
| CC | amino acid sequences. ABG00010-ABG3037 represent novel human |
| CC | diagnostic amino acid sequences of the invention. |
| CC | Note: The sequence data for this patent did not appear in the printed |
| CC | specification, but was obtained in electronic format directly from WIPO |
| CC | at ftp.wipo.int/pub/published_pcl_sequences. |
| XX | |
| SQ | Sequence 325 AA: |
| | |
| Query Match | 91.6%; Score 1417; DB 22; Length 325; |
| Best Local Similarity | 92.7%; Pred No. 1.3e-140; |
| Matches 280; Conservative | 3; Mismatches 15; Indels 4; Gaps 3 |
| OY | 1 WTDAAISFAKDFLAGVAAAIKSTAVAPIERVKLLDVOHASKOITADKOYGIIDCVVR 60 |
| Db | |
| 24 | MTPDAVSFAKDFLAGVAAAIKSTAVAPIERVKLLDVOHASKOITADKOYGIIDCVVR 83 |
| OY | 61 IPKEGEVLSFMRGNLANVIRFPPTQALNFAFDKKQTGLGSVDKRTQWRFFAGLASG 120 |
| Db | |
| 84 | IPKEGEVLSFMRGNLANVIRFPPTQALNFAFDKKQTGLGSVDKRTQWRFFAGLASG 143 |
| OY | 121 GAAGATSLCFPYPLDFARTRIADVGAKGAEREFGDLGDLTKVIYKSDSITKGLYGFNN 180 |
| Db | |
| 144 | GAGATSLCFPYPLDFARTRIADVGAKGAEREFGDLGDLTKVIYKSDSITKGLYGFNN 203 |
| OY | 181 VGGIITYRAAFGYIDTAKMLPDRKNTHIVYSMAIAQTV-TAVAGLSYEPDT--VRRR 237 |
| Db | |
| 204 | VGGIITYRAAFGYIDTAKMLPDRKNTHIVYSMAIAQTV-HCCCPXLLPEPTRSRVRRN 263 |
| OY | 238 MMMSGRGKTIDMTGTLDCKRKIKARDEGKAFFFGAMSNVLKMGAGAYLVLYD-EIRK 296 |
| Db | |
| 264 | EKMMSGRGKTIDMTGTLDCKRKIKARDEGKAFFFGAMSNVLKMGAGAYLVLYEAKSKR 323 |
| OY | 297 YTF 298 |
| Db | |
| 324 | YTF 325 |
| RESULT 11 | |
| AAM61169 | |
| ID | AAM61169 standard; Protein; 298 AA. |
| XX | |
| XX | AAM61169; |
| DT | 28-SEP-1998 (first entry) |
| XX | |
| XX | Anti1 protein. |
| KW | Anti1: Adenine nucleotide translocator; cloning; screening; |
| KW | DNA Tag diodeoxy terminator cycle sequencing; oxidative phosphorylation; |
| KW | probe; OXHOS; mitochondria; ADP; ATP; homozygous mutant; myopathy; |
| KW | hypertrophic cardiomyopathy; fascioscapular humeral muscular dystrophy; |
| KW | lactic acidosis; degenerative muscle disease. |
| XX | |
| MS | Mus sp. |

| XX | PN | MO9819714-A1. |
|----|--|----------------------------|
| XX | PD | 14-MAY-1998. |
| XX | XX | |
| XX | XX | 31-OCT-1997; 97MO-US19882. |
| XX | PF | |
| XX | PR | 01-NOV-1996; 96US-0030017. |
| XX | XX | |
| PA | (UYEM-) UNIV EMORY. | |
| PI | Graham BC, Macgregor GR, Wallace DC; | |
| XX | | |
| XX | WPI: 1998-286608/25. | |
| DR | N-PSDB; AAV36479. | |
| XX | | |
| PT | Mice lacking heart-muscle adenine nucleotide translocator protein - | |
| PT | useful as model for mitochondrial myopathy and hypertrophic | |
| PT | cardiomyopathy in animals and to test therapeutic compositions or | |
| PT | gene therapies | |
| XX | | |
| PS | Disclosure: Page 39-40; 61pp; English. | |
| CC | | |
| CC | The present sequence is the mouse Ant1 protein, the cDNA producing this | |
| CC | polypeptide is cloned by screening a mouse heart cDNA library with the | |
| CC | human Ant1 cDNA as a probe. The Ant1 cDNA sequence was determined by DNA | |
| CC | Tag dideoxy terminator cycle sequencing. The Ant1 protein is encoded by | |
| CC | the Ant1 locus, a nuclear gene on chromosome 8. This protein is required | |
| CC | in mitochondrial oxidative phosphorylation (OXPHOS), as it imports ADP | |
| CC | which can then be converted into ATP. An Ant1 homozygous mutant would | |
| CC | thus be defective in OXPHOS which results in disease in oxidative | |
| CC | metabolism dependent tissues. This mouse Ant1 homozygous mutant can be | |
| CC | used as a model system for fascioscapular humeral muscular dystrophy, | |
| CC | hypertrophic cardiomyopathy, myopathy, lactic acidosis, etc. These model | |
| CC | systems can be used to test possible therapeutic compounds which | |
| CC | increase/mediate ATP and ADP exchange across the mitochondrial membrane | |
| CC | independent of ANT1. | |
| XX | | |
| XX | Sequence 298 AA; | |
| XX | | |
| XX | Query Match 91.2%; Score 1411; DB 19; Length 298; | |
| XX | Best Local Similarity 89.2%; Pred. No. 4.9e-140; | |
| XX | Matches 265; Conservative 15; Mismatches 17; Indels 0; Gaps 0; | |
| QY | 1 MTDAALSAKQPLFAGVAAATSKTAVADIERVKLLQVOHASKQTADQYKGIIDCYVR 60 | |
| DB | 1 MGDDALSLPKLQPLFAGVAAATSKTAVADIERVKLLQVOHASKQTADQYKGIIDCYVR 60 | |
| QY | 61 IPKEQEVLSFMRGNLANVIRYEPQALVFARFKDKYKQFLGSDVRKQTFMRYPAGNLSG 120 | |
| DB | 61 IPKEQGLSLFMRGNLANVIRYEPQALVFARFKDKYKQFLGSDVRKQTFMRYPAGNLSG 120 | |
| QY | 121 GAAGATSLCFEYVPLDFARTFLAADVKGAGAEFERFGIDCLVKTIYKSDIGIKLYOGFNVS 180 | |
| DB | 121 GAAGATSLCFEYVPLDFARTFLAADVKGAGAEFERFGIDCLVKTIYKSDIGIKLYOGFNVS 180 | |
| QY | 181 VGGITIVAAAFGYDTPRAKGLMDPPKKNHIVISMMIAQTVAVAGLTSYPRPDYARRRRMM 240 | |
| DB | 181 VGGITIVAAAFGYDTPRAKGLMDPPKKNHIVISMMIAQTVAVAGLTSYPRPDYARRRRMM 240 | |
| QY | 241 QSGRKGTDIMVTGTLDCWRKLTARDEGGAFFKGAMSNVLRMGAGFVYLVDLTKKY 297 | |
| DB | 241 QSGRKGADIMVTGTLDCWRKLTAKDEGGAFFKGAMSNVLRMGAGFVYLVDLTKKY 297 | |
| XX | RESULT 12 | |
| XX | ABU53219 | |
| XX | ABU53219 standard; Protein: 293 AA. | |
| XX | ABU53219; | |
| XX | 14-APR-2003 (first entry) | |

| ID | AA | DT | DE |
|-----------|---|----|----|
| XX | Human metabolismm-associated DNFzphthes3_35n12 homologue #1. | | |
| XX | Human; gene therapy; vaccine; disease treatment; detection. | | |
| XX | Homo sapiens. | | |
| XX | Wo200112659-A2. | | |
| XX | 22-FEB-2001. | | |
| XX | 18-AUG-2000; 2000WO-IB01496. | | |
| XX | 18-AUG-1999; 99US-0149499. | | |
| XX | 28-SEP-1999; 99US-0156503. | | |
| XX | (GENU-) GERMAN HUMAN GENOME PROJECT. | | |
| XX | Wiemann S; | | |
| XX | WPI: 2001-327840/34. | | |
| XX | Nucleic acids having the sequences of clones isolated from libraries of different human tissues, useful in recombinant DNA methodologies - | | |
| XX | Example III; Page 850; 1095pp; English. | | |
| XX | This invention describes novel polynucleotides and polypeptides isolated from human cDNA libraries which can be used for gene therapy or in vaccines. The polynucleotides of the invention and antibodies encoded by CC them may be used in the prevention, diagnosis and treatment of diseases CC associated with inappropriate polypeptide expression. The products of the CC invention may also be used to identify modulators of expression and CC activity and to down regulate expression and activity. The antibodies of CC the invention may also be used as diagnostic agents for detecting the CC presence of polypeptides in samples. This sequence represents a homologue CC of a polypeptide described in the disclosure of the invention. | | |
| XX | Sequence 293 AA: | | |
| XX | Query Match 91.1%; Score 1409; DB 22; Length 293; | | |
| XX | Best Local Similarity 90.1%; Pred. No. 7.7e-140; | | |
| XX | Matches 264; Conservative 15; Mismatches 14; Indels 0; Gaps 0; | | |
| QY | 5 ALSTAKDFLAGGVAASIKTAIVAPIERYKLLQVOHASKQTADKQYGIIDCVRIKPE 64 | | |
| DB | 1 ALSTLKDFLAGGIAAASKTAVAPIERYKLLQVOHASKQISAEKQYGIIDCVRIKPE 60 | | |
| QY | 65 QEVLSFPMNGNLANIYRFPPTQALNPAFDKTKQIFLGVDNRTOFRFAGNLASGGAG 124 | | |
| DB | 61 QGVLSFPMNGNLANIYRFPPTQALNPAFDKTKQIFLGVDNRHOKPWRFFAGNLASGGAG 120 | | |
| QY | 125 ATSLCFYVPLDFAFTRILADADGKGAEREFEGLDCLVKIYKSDIGKLYOGFNYSVGI 184 | | |
| DB | 121 ATSLCFYVPLDFAFTRILADADGKSSQSEFEGLDCLVKIRKSDIGKLYOGFSVYGI 180 | | |
| QY | 185 IITYAAVFGIYDAKGMIPDEKNTNHIYSWMIAGTQVAVAGITSPEDTVRRMMQSGR 244 | | |
| DB | 181 IITYRAAFEGVYDTRAKGMLPDEKNTNHIYSWMIAGSVTAAGLVSYPEDTVRRMMQSGR 240 | | |
| QY | 245 KGTIDIMTGTLLDCWRKLTARDGGGAFFRGAMSNVLRGSGAFVLYLYEIKRY 297 | | |
| DB | 241 KGADIMYTGTLLDCWRKLTAKDEGANAFRGAMSNVLRGSGAFVLYLYDEIKRY 293 | | |
| RESULT 13 | | | |
| AA71031 | | | |
| ID | AA71031 standard; Protein: 297 AA. | | |
| XX | AA71031; | | |
| XX | 29-AUG-2000 (first entry) | | |
| XX | Human adenine nucleoside translocator ANTI. | | |
| DE | | | |

XX Human; adenine nucleotide translocator; ANT1; mitochondria; ADP; ATP;
 KW adenosine di-phosphate; adenosine tri-phosphate; apoptosis; MPT; cancer;
 KW mitochondrial permeability transition; neuroprotective; neurotropic;
 KW antiParkinsonian; cytoskeletal; antidiabetic; anticonvulsant; neuroleptic;
 KW antipsychotic; cerebroprotective; therapeutic; screening; psoriasis;
 KW Alzheimer's disease; Parkinson's disease; Huntington's disease; dystonia;
 KW diabetes; Leber's hereditary optic neuropathy; schizophrenia; MELAS;
 KW mitochondrial encephalopathy; lactic acidosis; stroke; MIDD;
 KW mitochondrial diabetes and deafness; hyperproliferative disorder;
 KW myoclonic epilepsy red ragged fibre syndrome.

OS Homo sapiens.

PN WO200026370-A2.

PD 11-MAY-2000.

PF 03-NOV-1999; 99WO-US25883.

PR 03-NOV-1998; 98US-0185904.

PR 08-SEP-1999; 99US-0393441.

XX (MITO-) MITOKOR.

PI Anderson CM, Davis RE, Clevenger W, Wiley SE, Miller SW, Szabo TR;
 PI Ghosh SS;

DR MPI: 2000-365619/31.

DR N-PSDB; AAD00519.

XX Recombinant construct encoding adenine nucleotide translocator
 PT polypeptide, useful e.g. in screening for potential therapeutic agents
 PT against mitochondrial disease

PS Claim 44; Page 172; 175pp; English.

XX The patent discloses a method to produce adenine nucleotide translocator
 CC (ANT) proteins or ANT fusion proteins using recombinant expression
 CC constructs. ANT is a nuclear encoded protein and a major component of
 CC inner mitochondrial membrane. It mediates transport of adenosine
 CC di/tri-phosphates across the mitochondrial inner membrane and also serves
 CC as an important molecular component of the mitochondrial permeability
 CC transition pore, a modulator of apoptosis. ANT is used to identify agents
 CC or ligands that bind to, or interact with it. The ANT ligands are used to
 CC detect or isolate ANT in a biological sample, and therapeutically for
 CC regulating mitochondrial pore activity, for treating diseases associated
 CC with altered mitochondrial function, including Alzheimer's, Parkinson's
 CC and Huntington's diseases, cancer, psoriasis, diabetes, dystonia,
 CC Leber's hereditary optic neuropathy, schizophrenia, mitochondrial
 CC encephalopathy, lactic acidosis and stroke (MELAS), hyperproliferative
 CC disorders, mitochondrial diabetes and deafness (MIDD), and myoclonic
 CC epilepsy red ragged fibre syndrome. The present sequence is an
 CC adenine nucleotide translocator ANT1 from human brain.

XX Sequence 297 AA:

Query Match 89.9%; Score 1391.5; DB 21; Length 297;

Best Local Similarity 88.6%; Pred. No. 5.5e-138;

Matches 263; Conservative 17; Mismatches 16; Indels 1; Gaps 1;

QY 1 MTDAALSPAKDFLAGVAAASIKTAVPIERVKLLQVQHASKOITADKOYGIIDCYVR 60

DB 1 MODHAMSFLKDFLAGVAAVAASKTAVPIERVKLLQVQHASKOISAEQYGIIDCYVR 60

QY 61 IPKEBVLSTFMGNLANVIRYPTQALNFAFDKTKQITFLGVDKRTOFWRRPAGNLSG 120

DB 61 IPKEBGLSTFMGNLANVIRYPTQALNFAFDKTKQITFLGVDKRTOFWRRPAGNLSG 120

QY 121 GAAGATSLCEFYVPLDFARTLADYDGAAREFGIGDCLATIKYSOSIKLTYGFNS 180

DB 121 GAAGATSLCEFYVPLDFARTLADYDGAAREFGIGDCLATIKYSOSIKLTYGFNS 179

QY 181 VGGIIIRAAFGIYDTAKGMLDPPKNTIIVISMIAQTVAAGITSTYPTVRRRMK 240
 DB 180 VGGIIIRAAFGIYDTAKGMLDPPKNTIIVISMIAQTVAAGITSTYPTVRRRMK 239

QY 241 QSGRGKTDIMTYGITLDCWRKIRADEGKAFEFYGANSNVRKMGAFVLYLDEIKKY 297
 DB 240 QSGRGKADIMTYGITLDCWRKIRADEGKAFEFYGANSNVRKMGAFVLYLDEIKKY 296

RESULT 14

AA001198

ID AAU01198 standard; Protein; 297 AA.

AC AAU01198;

DT 07-SEP-2001 (first entry)

DE Human adenine nucleotide translocator-1 (ANT-1) protein.

XX Human; adenine nucleotide translocator-1; ANT-1; MPT; cyclophilin;

KW mitochondrial permeability transition pore component; cell survival;

KW mitochondrial core component; mitochondrial related disorder; cancer;

KW Alzheimer's disease; diabetes mellitus; hyperproliferative disorder.

XX Homo sapiens.

PN WO200132876-A2.

PD 10-MAY-2001.

PF 03-NOV-2000; 2000WO-US30535.

PR 03-NOV-1999; 99US-0434354.

XX (MITO-) MITOKOR.

PI Murphy AN, Clevenger W, Wiley SE, Andreyev AY, Fritgerl LG;

PI Vellicelabi G, Davis RE;

DR MPI: 2001-291054/30.

DR N-PSDB; AAS05901.

XX New nucleic acid expression constructs, useful for screening for agents
 PT that alter mitochondrial permeability transition (MPT), comprises
 PT polynucleotide encoding MPT polypeptide or cyclophilin polypeptide
 PT fused to energy transfer molecule

XX Disclosure; Fig 2; 186pp; English.

XX The present sequence represents human adenine nucleotide translocator-1
 CC (ANT-1) protein. ANT proteins are mitochondrial permeability
 CC transition (MPT) pore components responsible for mediating transport
 CC of ADP across the mitochondrial inner membrane. ANT proteins interact
 CC with other mitochondrial core components e.g. cyclophilins to
 CC regulate MPT. The present invention relates to a novel nucleic acid
 CC expression construct comprising a promoter operably linked to a
 CC polynucleotide encoding a mitochondrial pore component polypeptide
 CC (e.g. ANT) fused to an energy transfer molecule (ETM) protein
 CC (e.g. green fluorescent protein (GFP) or a FLASH sequence). The novel
 CC expression construct can alter mitochondrial membrane permeability
 CC transition and/or alter the interaction between mitochondrial core
 CC components. The methods are useful for screening for agents that alter
 CC MPT and/or cell survival. These agents are useful for the prevention or
 CC treatment of diseases associated with altered mitochondrial function or
 CC dysfunction of cell survival, such as Alzheimer's disease, diabetes
 CC mellitus, Parkinson's disease, Huntington's disease, schizophrenia,
 CC mitochondrial encephalopathy, lactic acidosis, stroke,
 CC hyperproliferative disorders e.g. cancer, and deafness.

XX Sequence 297 AA:

Query Match 89.9%; Score 1391.5; DB 22; Length 297;

Best Local Similarity 88.6%; Pred. No. 5.5e-138;

Matches 263: Conservative 17; Mismatches 16; Indels 1; Gaps 1;

QY 1 MTDALSFADFLAGVAAAIKSTAVAPIERVKLLLOVHASKOITADKOYKGIIDCVR 60
 1 MGDHAWSFLLDFLAGVAAAVSKTAVAPIERVKLLLOVHASKOISAEKOYKGIIDCVR 60

Db 61 IPKQEVLSFRKGLAVIRFPFOALNFAFKDKYKQIFLGVDKRFQFRYFAGNLASG 120
 61 IPKQEVLSFRKGLAVIRFPFOALNFAFKDKYKQIFLGVDKRFQFRYFAGNLASG 120

QY 121 GAAGATSLCFVYPLDFARTRLAADVGRKAGAEERFGLGDLVKIKSDGIRKGLYQGFNV 180
 121 GAAGATSLCFVYPLDFARTRLAADVGRKAGAEERFGLGDLVKIKSDGIRKGLYQGFNV 180

Db 121 GAAGATSLCFVYPLDFARTRLAADVGRKAGAEERFGLGDLVKIKSDGIRKGLYQGFNV 179
 181 VQGIITRAAYFGIYDTAKGMLPDPKNTHTVISMIAQVYAVAGLTSYFEDVYRRMM 240
 180 VQGIITRAAYFGIYDTAKGMLPDPKNTHTVISMIAQVYAVAGLTSYFEDVYRRMM 239

QY 241 QSGRKGTDIMYTGILDCMRKRIARDEGKAFKFGKMSVNLGMSGAFVLYLYDEIKKY 297
 240 QSGRKGADIMYTGIVDCMRKRIARDEGKAFKFGKMSVNLGMSGAFVLYLYDEIKKY 296

RESULT 15

AAU10378 standard; Protein: 297 AA.

AAU10378:

14-FEB-2002 (first entry)

Human adenine nucleotide translocator 1 (ANT1).

Human; adenine nucleotide translocator; ANT;

mitochondrial matrix protein.

Homo sapiens.

W0200185944-A2.

15-NOV-2001.

11-MAY-2001; 2001MO-US15416.

11-MAY-2000; 2000US-0569327.

(MITO-) MITOKOR.

Anderson CM, Davis RE, Clevenger W, Wiley SE, Miller SM, Szabo TR;

Ghosh SS, Moos WH, Fel Y, Carroll AK;

WPI; 2002-055598/07.

N-PSDB; AAS16688.

Novel recombinant expression construct for producing adenine nucleotide

translocator polypeptides, comprises a regulated promoter linked to

nucleic acid encoding the polypeptide

Claim 44; Fig 2; 147pp; English;

The invention relates to a recombinant expression construct (I) comprising a regulated promoter operably linked to a nucleic acid encoding an adenine nucleotide translocator (ANT) polypeptide. ANT proteins mediate the exchange of ATP synthesised in the mitochondrial matrix for ADP in the cytosol. (I) is useful for producing recombinant ANT polypeptide by transforming a prokaryotic or eukaryotic host cell and culturing the host cell. (I) is also useful for targeting a polypeptide of interest to a mitochondrial membrane, where ANT polypeptide is expressed as a fusion protein with the polypeptide of interest. Recombinant ANT polypeptide, or cells expressing the polypeptide, is useful for identifying an agent that binds to an ANT polypeptide. ANT ligand is useful for determining the presence of an ANT polypeptide, preferably ANTI, ANT2 or ANT3 in a biological sample and for isolating

CC ANT from a biological sample, where the ANT ligand is covalently or non-covalently bound to a solid phase. Detectably labeled ANT ligand is also useful for identifying an agent that interacts with an ANT polypeptide. The present sequence represents the amino acid sequence of human ANTI.

Sequence 297 AA;

Query Match 89.9%; Score 1391.5; DB 23; Length 297;

Best local similarity 88.6%; Pred. No. 5.5e-138;

Matches 263; Conservative 17; Mismatches 16; Indels 1; Gaps 1;

QY 1 MTDALSFADFLAGVAAAIKSTAVAPIERVKLLLOVHASKOITADKOYKGIIDCVR 60
 1 MGDHAWSFLLDFLAGVAAAVSKTAVAPIERVKLLLOVHASKOISAEKOYKGIIDCVR 60

Db 61 IPKQEVLSFRKGLAVIRFPFOALNFAFKDKYKQIFLGVDKRFQFRYFAGNLASG 120
 61 IPKQEVLSFRKGLAVIRFPFOALNFAFKDKYKQIFLGVDKRFQFRYFAGNLASG 120

QY 121 GAAGATSLCFVYPLDFARTRLAADVGRKAGAEERFGLGDLVKIKSDGIRKGLYQGFNV 180
 121 GAAGATSLCFVYPLDFARTRLAADVGRKAGAEERFGLGDLVKIKSDGIRKGLYQGFNV 179

Db 121 GAAGATSLCFVYPLDFARTRLAADVGRKAGAEERFGLGDLVKIKSDGIRKGLYQGFNV 179
 181 VQGIITRAAYFGIYDTAKGMLPDPKNTHTVISMIAQVYAVAGLTSYFEDVYRRMM 240
 180 VQGIITRAAYFGIYDTAKGMLPDPKNTHTVISMIAQVYAVAGLTSYFEDVYRRMM 239

QY 241 QSGRKGTDIMYTGILDCMRKRIARDEGKAFKFGKMSVNLGMSGAFVLYLYDEIKKY 297
 240 QSGRKGADIMYTGIVDCMRKRIARDEGKAFKFGKMSVNLGMSGAFVLYLYDEIKKY 296

Search completed: August 28, 2003, 19:38:48

Job time : 53.3919 secs

GenCore version 5.1.6
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OM protein - protein search, using SW model

Run on: August 28, 2003, 19:36:11 ; Search time 18.0202 Seconds
(without alignments)
699.696 Million cell updates/sec

Title: US-09-811-132-32

Perfect score: 1547
Sequence: 1 MTDALSPAKDFLAGVAAA.....LRGMGAFVLVLYDEIKRYT 298

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 328717 seqs, 42310858 residues

Total number of hits satisfying chosen parameters: 328717

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA.*

1: /cgn2_6/ptodata/1/1aa/5A.COMB.pep:*
2: /cgn2_6/ptodata/1/1aa/5B.COMB.pep:*
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4: /cgn2_6/ptodata/1/1aa/6B.COMB.pep:*
5: /cgn2_6/ptodata/1/1aa/PCRTS.COMB.pep:*
6: /cgn2_6/ptodata/1/1aa/Backfile1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|--------|-------------|--------|----|--------------------|
| 1 | 1547 | 100.0 | 298 | 4 | US-09-434-354-48 |
| 2 | 1454 | 94.0 | 298 | 4 | US-09-434-354-49 |
| 3 | 1411 | 91.2 | 298 | 3 | US-08-961-871-10 |
| 4 | 1391.5 | 89.9 | 297 | 4 | US-09-434-354-47 |
| 5 | 302 | 19.5 | 469 | 4 | US-09-996-243-289 |
| 6 | 301 | 19.5 | 469 | 3 | US-09-188-930-339 |
| 7 | 301 | 19.5 | 469 | 4 | US-09-312-283C-339 |
| 8 | 274 | 17.7 | 291 | 4 | US-09-501-558-2 |
| 9 | 274 | 17.7 | 335 | 4 | US-09-482-273-118 |
| 10 | 261.5 | 16.9 | 447 | 4 | US-09-160-119-4 |
| 11 | 261.5 | 16.9 | 674 | 4 | US-09-160-119-4 |
| 12 | 247 | 16.0 | 312 | 3 | US-09-142-565-2 |
| 13 | 244.5 | 15.8 | 311 | 2 | US-08-775-009-33 |
| 14 | 239.5 | 15.5 | 309 | 1 | US-08-518-878B-51 |
| 15 | 239.5 | 15.5 | 309 | 2 | US-08-807-861A-51 |
| 16 | 239.5 | 15.5 | 309 | 2 | US-08-470-868A-51 |
| 17 | 239.5 | 15.5 | 309 | 3 | US-08-210-681-51 |
| 18 | 239.5 | 15.5 | 309 | 4 | US-08-946-719A-51 |
| 19 | 239.5 | 15.5 | 309 | 4 | US-08-547-983-51 |
| 20 | 236.5 | 15.3 | 299 | 1 | US-08-518-878B-56 |
| 21 | 236.5 | 15.3 | 299 | 2 | US-08-470-868A-56 |
| 22 | 232.5 | 13.0 | 311 | 2 | US-08-775-009-32 |
| 23 | 230.5 | 14.9 | 320 | 3 | US-08-933-750C-12 |
| 24 | 230.5 | 14.9 | 320 | 3 | US-09-234-613-12 |
| 25 | 227 | 14.7 | 308 | 2 | US-08-937-466-2 |
| 26 | 227 | 14.7 | 308 | 2 | US-09-172-528-2 |
| 27 | 227 | 14.7 | 308 | 3 | US-09-318-199-6 |

| | | | | | | |
|----|-------|------|-----|---|-------------------|-------------------|
| 28 | 227 | 14.7 | 308 | 3 | US-09-503-579-2 | Sequence 2, Appl |
| 29 | 223 | 14.4 | 432 | 2 | US-08-937-466-4 | Sequence 4, Appl |
| 30 | 223 | 14.4 | 432 | 2 | US-09-172-528-4 | Sequence 4, Appl |
| 31 | 223 | 14.4 | 432 | 3 | US-09-318-199-4 | Sequence 4, Appl |
| 32 | 223 | 14.4 | 432 | 3 | US-09-503-579-4 | Sequence 4, Appl |
| 33 | 219.5 | 14.2 | 293 | 4 | US-09-501-558-4 | Sequence 4, Appl |
| 34 | 218.5 | 14.1 | 303 | 1 | US-08-294-522B-36 | Sequence 36, Appl |
| 35 | 217.5 | 14.1 | 303 | 1 | US-08-518-878B-37 | Sequence 37, Appl |
| 36 | 217.5 | 14.1 | 303 | 2 | US-08-807-861A-37 | Sequence 37, Appl |
| 37 | 217.5 | 14.1 | 303 | 2 | US-08-470-868A-37 | Sequence 37, Appl |
| 38 | 217.5 | 14.1 | 303 | 3 | US-09-210-681-37 | Sequence 37, Appl |
| 39 | 217.5 | 14.1 | 303 | 3 | US-08-946-719A-37 | Sequence 37, Appl |
| 40 | 217.5 | 14.1 | 303 | 4 | US-09-547-983-37 | Sequence 37, Appl |
| 41 | 191 | 12.3 | 328 | 3 | US-09-068-140A-15 | Sequence 15, Appl |
| 42 | 190.5 | 12.3 | 256 | 2 | US-08-937-466-6 | Sequence 6, Appl |
| 43 | 190.5 | 12.3 | 256 | 2 | US-09-172-528-6 | Sequence 6, Appl |
| 44 | 190.5 | 12.3 | 256 | 3 | US-09-318-199-6 | Sequence 6, Appl |
| 45 | 190.5 | 12.3 | 256 | 3 | US-09-503-579-6 | Sequence 6, Appl |

ALIGNMENTS

RESULT 1
US-09-434-354-48
Sequence 48, Application US/09434354

Patent No. 6562563

GENERAL INFORMATION:

APPLICANT: Murphy, Anne N.

APPLICANT: Cleveneger, William

APPLICANT: Wiley, Sandra Eileen

APPLICANT: Andreyev, Alexander Y.

APPLICANT: Frigieri, Luciano G.

APPLICANT: Velicelab, Gonul

APPLICANT: Davis, Robert E.

TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETERMINING

TITLE OF INVENTION: INTERACTIONS OF MITOCHONDRIAL COMPONENTS, AND FOR

TITLE OF INVENTION: IDENTIFYING AGENTS THAT ALTER SUCH INTERACTIONS

FILE REFERENCE: 660088.433

CURRENT FILING DATE: 1999-11-03

NUMBER OF SEQ ID NOS: 54

SOFTWARE: FastSeq for Windows Version 3.0

SEQ ID NO 48

LENGTH: 298

TYPE: PRT

ORGANISM: Homo sapien

US-09-434-354-48

Query Match
Best Local Similarity 100.0%; Score 1547; DB 4; Length 298;
Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

| | | | |
|----|-----|--|-----|
| QY | 1 | MTDALSPAKDFLAGVAAAISKTAVAPIERVKLLQVOHASKQITADQYKGIIDCVVR | 60 |
| DB | 1 | MTDALSPAKDFLAGVAAAISKTAVAPIERVKLLQVOHASKQITADQYKGIIDCVVR | 60 |
| QY | 61 | IPEDQVLSFWKGNLANVRYPTQALNFAFDKYOITLGGVDKTOFWRRFAGNLAGS | 120 |
| DB | 61 | IPEDQVLSFWKGNLANVRYPTQALNFAFDKYOITLGGVDKTOFWRRFAGNLAGS | 120 |
| QY | 121 | GAAGATSLCFVYPLDFARTRLADYVAKAGAEFRGLDCLVITYKSDGIGKYOGFNYS | 180 |
| DB | 121 | GAAGATSLCFVYPLDFARTRLADYVAKAGAEFRGLDCLVITYKSDGIGKYOGFNYS | 180 |
| QY | 181 | VGGIIRYRAVYGIYDTAKGMLPDPKNTIIVISWMAQVTVAVAGLTSVPDTRRRMM | 240 |
| DB | 181 | VGGIIRYRAVYGIYDTAKGMLPDPKNTIIVISWMAQVTVAVAGLTSVPDTRRRMM | 240 |
| QY | 241 | OSGRKGTDMYGTGLDCMKRIARDEGKAFPGKAMSNVLRGMGAFVLVLYDEIKRYT | 298 |
| DB | 241 | OSGRKGTDMYGTGLDCMKRIARDEGKAFPGKAMSNVLRGMGAFVLVLYDEIKRYT | 298 |

```

RESULT 2
US-09-434-354-49
; Sequence 49, Application US/09434354
; Patent No. 6562563
; GENERAL INFORMATION:
; APPLICANT: Murphy, Anne N.
; APPLICANT: Clewenger, William
; APPLICANT: Wiley, Sandra Eileen
; APPLICANT: Andreyev, Alexander Y.
; APPLICANT: Frigeri, Luciano G.
; APPLICANT: Vellicoleli, Gonul
; APPLICANT: Davis, Robert E.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETERMINING
; TITLE OF INVENTION: INTERACTIONS OF MITOCHONDRIAL COMPONENTS, AND FOR
; FILE REFERENCE: 660088.433
; CURRENT APPLICATION NUMBER: US/09/434,354
; CURRENT FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 49
; LENGTH: 298
; TYPE: prt
; ORGANISM: Homo sapien
US-09-434-354-49

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|-----------------------|------------------|---------------------|-----------|-------------|
| Query Match | 94.08; | Score 1454; | DB 4; | Length 298; |
| Best Local Similarity | 92.68; | Pred. NO. 6.3e-159; | | |
| Matches 274; | Conservative 13; | Mismatches 9; | Indels 0; | Gaps 0; |

[illegible]

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1      RESULT 3
2      US-08-961-871-10
3      Sequence 10, Application US/08961871
4      Patent No. 601858
5      GENERAL INFORMATION:
6      APPLICANT: Wallace, Douglas C.
7      APPLICANT: Graham, Brett H.
8      APPLICANT: Macgregor, Grant R.
9      TITLE OF INVENTION: Mouse Lacking Heart-Muscle Adenine
10     NUCLEOTIDE TRANSLATOR PROTEIN AND METHODS
11     NUMBER OF SEQUENCES: 11
12     CORRESPONDENCE ADDRESS:
13     ADDRESSEE: Greenlee, Winner and Sullivan, P. C.
14     STREET: 5370 Manhattan Circle, Suite 201
15     CITY: Boulder
16     STATE: Colorado
17     COUNTRY: US
18     ZIP: 80303
19     COMPUTER READABLE FORM:
20     MEDIUM TYPE: Floppy disk
21     COMPUTER: IBM PC compatible

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```

OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,871
FILING DATE: 31-OCT-1997
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/030,017
FILING DATE: 01-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Ferber, Donna M.
REGISTRATION NUMBER: 33, 78-8
REFERENCE/DOCKET NUMBER: 78-96
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 499-8080
TELEFAX: (303) 499-8089
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 298 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-961-871-10

```

| | | | | |
|-----------------------|------------------|---------------------|-----------|-------------|
| Query Match | 91.28; | Score 1411; | DB 3; | Length 298; |
| Best Local Similarity | 89.28; | Pred. No. 5.6e-154; | | |
| Matches 265; | Conservative 15; | Mismatches 17; | Indels 0; | Gaps 0; |

| | | | |
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| QY | 1 | MTDAALSPAKDFLAGGVAALAASTKTAAPRIEHWKLLLYQVHNSKOTAPQKYGKIIDCYVR | 60 |
| Db | 1 | MGDALSFINDFLANGSLAANAASKTAAPRIEHWKLLLYQVHNSKOTAPQKYGKIIDCYVR | 60 |
| QY | 61 | IPKQEWLSPWRGMLANVIRYEPPOALNFAFKDKYKQIFLGGVDKPRQFMWYFAGNLASG | 120 |
| Db | 61 | IPKQGGELSPWRGMLANVIRYEPPOALNFAFKDKYKQIFLGGVDNRHKKQFMWYFAGNLASG | 120 |
| QY | 121 | GAAGATSLCFPYPLDFARTRLAADVYNGKGAERERGGJDCDYKTYKSGITGTLVGQFVAYS | 180 |
| Db | 121 | GAAGATSLCFPYPLDFARTTLAADVYNGKSSORERNGLDCLTKTKFKSGLGLVQGFVSVS | 180 |
| QY | 181 | VGGIIIVRAAYFGIYDTAKGMLPDPKNTHIYISMWIAQVYTAVALGVSYPEDTVARRRMM | 240 |
| Db | 181 | VGGIIIVRAAYFGVYDTAKGMLPDPKNVHIIVSWIAQSVTAVALGVSYPEDTVARRRMM | 240 |
| QY | 241 | QSGRKGADIMWTGTLDDCKRLTARBEGGAFKFGAMSNVLRMGCAFVLVYLDELTKY | 297 |
| Db | 241 | QSGRKGADIMWTGTLDDCKRLTAKGEGAAEFKFGAMSNVLRMGCAFVLVYLDELTKY | 297 |

```

RESULT 4
US-09-434-354-47
Sequence 47, Application US/09434354
Patent NO. 6562563
GENERAL INFORMATION:
APPLICANT: Murphy, Anne N.
APPLICANT: Clevenger, William
APPLICANT: Wiley, Sandra Eileen
APPLICANT: Andreyev, Alexander Y.
APPLICANT: Frigeri1, Luciano G.
APPLICANT: Velicel1, Gonul
APPLICANT: Davis, Robert E.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETERMINING
TITLE OF INVENTION: INTERACTIONS OF MITOCHONDRIAL COMPONENTS, AND FOR
TITLE OF INVENTION: IDENTIFYING AGENTS THAT ALTER SUCH INTERACTIONS
FILE REFERENCE: 660088,433
CURRENT APPLICATION NUMBER: US/09/434,354
CURRENT FILING DATE: 1999-11-03
NUMBER OF SEQ ID NOS: 54
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 47
LENGTH: 297
TYPE: PRT
ORGANISM: Homo sapien

```

US-09-434-354-47

Query Match 89.9%; Score 1391.5; DB 4; Length 297;
 Best Local Similarity 88.6%; Pred. No. 9,8e-152;
 Matches 263; Conservative 17; Mismatches 16; Indels 1; Gaps 1;

QY 1 MTDAALSPADFLAGVAAAIKTAAPVPIEYKLLLOVHASKOITADKQYGIIDCVR 60
 1 MGDHMSFLKDFLGAVAASKTAVAPIERVKLLLOVHASKOISAEKQYGIIDCVR 60
 QY 61 IPKQEVLSFWRGLNANVIREPTQALNFAKDKYKQIFLGVDVKRQFMVYFAGNLASG 120
 61 IPKQEVLSFWRGLNANVIREPTQALNFAKDKYKQIFLGVDVKRQFMVYFAGNLASG 120
 QY 121 GAAGATSLCEVYPLDFATRIADVGKAGAEFEFGSLDCLVKTIYKSDIGLQVGFVNS 180
 121 GAAGATSLCEVYPLDFATRIADVGRR-KQREFHGLDCLIKTFKSDIGLQVGFVNS 179
 Db 180 VQGIITRAAFYGYDFAKGLPDPKNVHIFVSWMIGSVYAVAGLLSYPDYARRMM 239
 181 VQGIITRAAFYGYDFAKGLPDPKNTHIVISMIAQTVTAVAGLSYPPDYARRMM 240
 QY 241 QSGRKGDIMYTGILDCRRKARDEGGKAFKAGMSNTLRMGAFVLYVDEIKKY 297
 240 QSGRKGDIMYTGIVDCWRKIAKDEGAKAFKAGMSNTLRMGAFVLYVDEIKKY 296

RESULT 5

US-09-996-243-289
 Sequence 289, Application US/09996243

Patent No. 6478825

GENERAL INFORMATION:

APPLICANT: Ashkenazi, Avi J.

APPLICANT: Baker, Kevin P.

APPLICANT: Botstein, David

APPLICANT: Desnoyers, Luc

APPLICANT: Eaton, Dan L.

APPLICANT: Ferrara, Napoleone

APPLICANT: Fong, Sherman

APPLICANT: Gerber, Hanspeter

APPLICANT: Gerritsen, Mary E.

APPLICANT: Goddard, Audrey

APPLICANT: Godowski, Paul J.

APPLICANT: Grimaldi, J. Christopher

APPLICANT: Gurney, Austin L.

APPLICANT: Kljavin, Ivar J.

APPLICANT: Napier, Mary A.

APPLICANT: Pan, James

APPLICANT: Paoni, Nicholas F.

APPLICANT: Roy, Margaret Ann

APPLICANT: Stewart, Timothy A.

APPLICANT: Tumas, Daniel

APPLICANT: Watanabe, Colin K.

APPLICANT: Williams, P. Mickey

APPLICANT: Wood, William I.

APPLICANT: Zhang, Zemin

TITLE OF INVENTION: Secreted and Transmembrane Polypeptides and Nucleic

TITLE OF INVENTION: Acids Encoding the Same

FILE REFERENCE: P2730P1C3

CURRENT APPLICATION NUMBER: US/09/996,243

PRIOR FILING DATE: 2001-11-14

PRIOR APPLICATION NUMBER: 60/049787

PRIOR FILING DATE: 1997-06-16

PRIOR APPLICATION NUMBER: 60/062250

PRIOR FILING DATE: 1997-10-17

PRIOR APPLICATION NUMBER: 60/065186

PRIOR FILING DATE: 1997-11-12

PRIOR APPLICATION NUMBER: 60/065311

PRIOR FILING DATE: 1997-11-13

PRIOR APPLICATION NUMBER: 60/066770

PRIOR FILING DATE: 1997-11-24

PRIOR APPLICATION NUMBER: 60/075945

PRIOR FILING DATE: 1998-02-25

PRIOR APPLICATION NUMBER: 60/078910
 PRIOR FILING DATE: 1998-03-20
 PRIOR APPLICATION NUMBER: 60/083322
 PRIOR FILING DATE: 1998-04-28
 PRIOR APPLICATION NUMBER: 60/084600
 PRIOR FILING DATE: 1998-05-07
 PRIOR APPLICATION NUMBER: 60/087106
 PRIOR FILING DATE: 1998-05-28
 PRIOR APPLICATION NUMBER: 60/087607
 PRIOR FILING DATE: 1998-06-02
 PRIOR APPLICATION NUMBER: 60/087609
 PRIOR FILING DATE: 1998-06-02
 PRIOR APPLICATION NUMBER: 60/087759
 PRIOR FILING DATE: 1998-06-02
 PRIOR APPLICATION NUMBER: 60/087827
 PRIOR FILING DATE: 1998-06-03
 PRIOR APPLICATION NUMBER: 60/088021
 PRIOR FILING DATE: 1998-06-04
 PRIOR APPLICATION NUMBER: 60/088025
 PRIOR FILING DATE: 1998-06-04
 PRIOR APPLICATION NUMBER: 60/088026
 PRIOR FILING DATE: 1998-06-04
 PRIOR APPLICATION NUMBER: 60/088028
 PRIOR FILING DATE: 1998-06-04
 PRIOR APPLICATION NUMBER: 60/088029
 PRIOR FILING DATE: 1998-06-04
 PRIOR APPLICATION NUMBER: 60/088030
 PRIOR FILING DATE: 1998-06-04
 PRIOR APPLICATION NUMBER: 60/088033
 PRIOR FILING DATE: 1998-06-04
 PRIOR APPLICATION NUMBER: 60/088326
 PRIOR FILING DATE: 1998-06-04
 PRIOR APPLICATION NUMBER: 60/088167
 PRIOR FILING DATE: 1998-06-05
 PRIOR APPLICATION NUMBER: 60/088202
 PRIOR FILING DATE: 1998-06-05
 PRIOR APPLICATION NUMBER: 60/088212
 PRIOR FILING DATE: 1998-06-05
 PRIOR APPLICATION NUMBER: 60/088217
 PRIOR FILING DATE: 1998-06-05
 PRIOR APPLICATION NUMBER: 60/088655
 PRIOR FILING DATE: 1998-06-09
 PRIOR APPLICATION NUMBER: 60/088734
 PRIOR FILING DATE: 1998-06-10
 PRIOR APPLICATION NUMBER: 60/088738
 PRIOR FILING DATE: 1998-06-10
 PRIOR APPLICATION NUMBER: 60/088742
 PRIOR FILING DATE: 1998-06-10
 PRIOR APPLICATION NUMBER: 60/088810
 PRIOR FILING DATE: 1998-06-10
 PRIOR APPLICATION NUMBER: 60/088824
 PRIOR FILING DATE: 1998-06-10
 PRIOR APPLICATION NUMBER: 60/088826
 PRIOR FILING DATE: 1998-06-10
 PRIOR APPLICATION NUMBER: 60/088858
 PRIOR FILING DATE: 1998-06-11
 PRIOR APPLICATION NUMBER: 60/088861
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 PRIOR APPLICATION NUMBER: 60/088876
 PRIOR FILING DATE: 1998-06-11
 PRIOR APPLICATION NUMBER: 60/089105
 PRIOR FILING DATE: 1998-06-12
 PRIOR APPLICATION NUMBER: 60/089440
 PRIOR FILING DATE: 1998-06-16
 PRIOR APPLICATION NUMBER: 60/089512
 PRIOR FILING DATE: 1998-06-16
 PRIOR APPLICATION NUMBER: 60/089514
 PRIOR FILING DATE: 1998-06-16
 PRIOR APPLICATION NUMBER: 60/089532
 PRIOR FILING DATE: 1998-06-17
 PRIOR APPLICATION NUMBER: 60/089538
 PRIOR FILING DATE: 1998-06-17
 PRIOR APPLICATION NUMBER: 60/089598

DB 293 IAOSITVMEVLTNRMA--LRKTG---OYSGMLDCARILLAKEGVAAPYKGIYPMGLIT 347
OY 186 IYRAAFGIYDPKAGMLDPKNTHT-----VISMIAQVTAAG-LTSYPRDT 233
DB 348 PYAGIDLAIVETL-----KNTWQRYAVNSADGCVVLLACGIISSITCGGLASYPAL 400
OY 234 VRRMMQSGRKGTIDIMYTGTLDCWRKIARDEGKAFFKAMSVNLRMGAFV-LVLYD 292
DB 401 VRTMQAQSIEGAPETVMSSL--FKQILRTGAGLYRGLAPNFMKVIAPAVISYVYE 458
OY 293 EIK 295
DB 459 NLK 461

RESULT 7

US-09-312-283C-339
; Sequence 339, Application US/09312283C
; Patent No. 6573095
; GENERAL INFORMATION:
; APPLICANT: Watson, James D.
; APPLICANT: Strachan, Lorna
; APPLICANT: Sleeman, Matthew
; APPLICANT: Orust, Rene
; APPLICANT: Murison, James G.
; TITLE OF INVENTION: Compositions Isolated from Skin Cells
; TITLE OF INVENTION: and Methods for Their Use
; FILE REFERENCE: 11000.1011c2
; CURRENT APPLICATION NUMBER: US/09/312,283C
; NUMBER OF SEQ ID NOS: 425
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 339
; LENGTH: 469
; TYPE: PRF
; ORGANISM: Mouse
US-09-312-283C-339

Query Match 19.5%; Score 301; DB 4; Length 469;
Best Local Similarity 28.4%; Pred. No. 7e-26;

Matches 86; Conservative 62; Mismatches 109; Indels 46; Gaps 12;

OY 10 KDLAAGVAAISKTAVPIERVKLLLOVHASQITADKQYKGIIDCV---RIPKEO 65
DB 188 RHLVAGGAGAVSRCTAPDLRLKVLQOV--HASSNNM-----CIVGFTGMINRG 237
OY 66 EVLSWRGNLANVIRFPTQALNFAFKDKYKQIFLGVDKRTQFRRYRAGNLASGGAAGA 125
DB 238 GAKSLMRNGINVLKIAPESAIKFMAYQMKR--LVGSDQET--LRHERLVAGSLAGA 292
OY 126 TSLCFVYPLDFARTRILADVGKAGAREFRGLDCLVYIKSGDKIGLYQGFVNSVOGII 185
DB 293 IAOSITVMEVLTNRMA--LRKTG---OYSGMLDCARILLAKEGVAAPYKGIYPMGLIT 347
OY 186 IYRAAFGIYDPKAGMLDPKNTHT-----VISMIAQVTAAG-LTSYPRDT 233
DB 348 PYAGIDLAIVETL-----KNTWQRYAVNSADGCVVLLACGIISSITCGGLASYPAL 400
OY 234 VRRMMQSGRKGTIDIMYTGTLDCWRKIARDEGKAFFKAMSVNLRMGAFV-LVLYD 292
DB 401 VRTMQAQSIEGAPETVMSSL--FKQILRTGAGLYRGLAPNFMKVIAPAVISYVYE 458
OY 293 EIK 295
DB 459 NLK 461

RESULT 8
US-09-501-558-2
; Sequence 2, Application US/09501558
; Patent No. 6403784
; GENERAL INFORMATION:

; APPLICANT: Turner, C. Alexander Jr.
; APPLICANT: Mathur, Brian
; APPLICANT: Zambrowicz, Brian
; APPLICANT: Sands, Arthur E.
; TITLE OF INVENTION: No. 6403784e1 Human Uncoupling Proteins and
; TITLE OF INVENTION: Polynucleotides Encoding the Same
; FILE REFERENCE: Lex-0012-USA
; CURRENT APPLICATION NUMBER: US/09/501,558
; CURRENT FILING DATE: 2000-02-09
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 291
; TYPE: PRF
; ORGANISM: Homo sapiens
US-09-501-558-2

Query Match 17.7%; Score 274; DB 4; Length 291;
Best Local Similarity 27.8%; Pred. No. 4.3e-23;

Matches 85; Conservative 55; Mismatches 134; Indels 32; Gaps 9;

OY 4 AALSFAKDELFGVAAISKTAVPIERVKLLLOVHAS-----KQITADKQYKGIIDCV 58
DB 2 SALNM--KRPVYGGIASTAECGTFPIDLTKTRIQOTNDKKEI---RYRGMHLAL 56
OY 59 VAIRPEQEVLSFWRGNLANVIRFPTQALNFAFKDKYKQIFLGVDKRTQFRRYRAGNL 118
DB 57 VAIRGEQKALYSGIAPMLAQASYGTIKITQYSLRFLEREDF-----LPINVI 111
OY 119 SGGAAGNSLCFVYPLDFARTRILADVGKAGAREFRGLDCLVYIKSGDKIGLYQGFN 178
DB 112 CGILSGVISSTIANPTDVLKIRMQAQSNTIQG-----CGWGNFMNINYOQEGTRGLMKGV 166
OY 179 VSVQGIITIRAFVFGYDPAK-----GMLDPKNTHTYISMIAQVTAAGLTSYPRD 232
DB 167 LTAORAAIVGVLPYDIDTKRHLILSGMLGTVYTHFSF---TCGLAALASNPVD 222
OY 233 TVRRMMQSG--RKGTIDIMYTGTLDCWRKIARDEGKAFFKAMSVNLR--GMGAFVLYL 290
DB 223 VRTMQAQSIEGAPETVMSSL--FKQILRTGAGLYRGLAPNFMKVIAPAVISYVYE 458
OY 291 YDEIKK 296
DB 283 YQLKK 288

RESULT 9

US-09-482-273-118
; Sequence 118, Application US/09482273
; Patent No. 6534631

; GENERAL INFORMATION:

; APPLICANT: Rosen et al.
; TITLE OF INVENTION: 71 Human Secreted Proteins

; FILE REFERENCE: P2030P1
; CURRENT APPLICATION NUMBER: US/09/482,273

; EARLIER FILING DATE: 2000-01-13
; EARLIER FILING DATE: 1999-07-14

; EARLIER FILING DATE: 1998-07-15
; EARLIER FILING DATE: 1998-07-15

; EARLIER FILING DATE: 1998-07-15
; EARLIER FILING DATE: 1998-07-15

; EARLIER FILING DATE: 1998-07-15
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; EARLIER FILING DATE: 1998-07-15
; EARLIER FILING DATE: 1998-07-15

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; EARLIER FILING DATE: 1998-07-15
; EARLIER FILING DATE: 1998-07-15

SEQ ID NO 2
LENGTH: 312
TYPE: PRT
ORGANISM: HOMO SAPIEN
US-09-142-565-2

Query Match 16.0%: Score 247; DB 3; Length 312;
Best Local Similarity 24.8%; Pred. No. 6,2e-20;
Matches 76; Conservative 56; Mismatches 149; Indels 26; Gaps 8;

QY 2 TDAALSPAKDFLACGVAATSKTAVAPIERVKLLQVQHASKQTLADK--QYKGLIDCV 59
DB 7 SDVPTAAVFKLGGTACFADLTFTPLDTAKVRLQIGENQAAVQTALVYRGVLTLL 66
QY 60 RIRPEQELSEFWRGNLANVRYPTQALNFAFKDKRYKQIFL--GGVDKRTQFWRFYAGNLA 118
DB 67 TMVTEPCSPYNGVLVGLQMSFASIRIGLYDSVQVYPRKADNSLTLTLLA----- 122
QY 119 SGAAGATSLCTFYPLDFARLADV--GKAGAEERERGLDCLVKYKSDGKGLYOG 176
DB 123 -GCTTGAAVYCAQPTDVVKVRFQASIHLPSSRSDKXSGTMDAYRTIAREEGVYGLMKG 181
QY 177 FNVSVGIIYRAVYFGIDYFAK-----GMLPDPKNTHIYISMMIAQTVTAVALGTSYP 230
DB 182 TLPIMRNALVNCLEVVYTYDILKEKLDYHLTDNPFCHFSAGAGCATVVAS---P 237
QY 231 FDTVRRMMQSGRRKGTDMYTGTLDCWRKIARDEGKAFPKGAMSNVLR--GMGAFVLY 289
DB 238 VDVKTRVYM-----NSPPGQYFSPLDCKIMKVAQEGPAFYKGTTPSLRLGSMNVVAFV 292
QY 290 LYDEIKR 296
DB 293 TYEQILKR 299

RESULT 13

US-08-775-009-33
Sequence 33, Application US/08775009
Patent No. 5935783

GENERAL INFORMATION:
APPLICANT: Gong, Wellong
APPLICANT: Emanuel, Beverly S.
APPLICANT: Budarf, Marcia L.
TITLE OF INVENTION: No. 5935783el Genes Mapping in the Digestion and
TITLE OF INVENTION: Velocardiofacial Syndrome Minimal Critical Region
NUMBER OF SEQUENCES: 45
CORRESPONDENCE ADDRESS:
ADDRESSEE: Woodcock Washburn Kurtz Mackiewicz &
ADDRESSEE: No. 5935783is, LLP
STREET: One Liberty Place - 46th Floor
CITY: Philadelphia
STATE: PA
COUNTRY: U.S.A.
ZIP: 19103

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/775,009
FILING DATE: 27-DEC-1996
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Trujillo, Doreen Yanko
REGISTRATION NUMBER: 35,719
REFERENCE/DOCKET NUMBER: CH-0681
TELECOMMUNICATION INFORMATION:
TELEPHONE: (215) 568-3100
TELEFAX: (215) 568-3439
INFORMATION FOR SEQ ID NO: 33:
SEQUENCE CHARACTERISTICS:

LENGTH: 311 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-775-009-33

Query Match 15.8%: Score 244.5; DB 2; Length 311;
Best Local Similarity 28.1%; Pred. No. 1,2e-19;
Matches 83; Conservative 47; Mismatches 138; Indels 27; Gaps 8;

QY 10 KDFLAGVAAAIKTAAPIERVKLLQVQHASKQTLADKQYKGLIDCVIRPEQEVLS 69
DB 27 KALLAGLAGIEICITPTPEYVKTOQLDERAN---PPRYRGIGDVRQTVRSHTVIG 82
QY 70 FWRGNLANVRYPTQALNFA---FKDKYKQIFLGVDKRTQFWRFYAGNLAASGAAGAT 126
DB 83 LYRGLSSLLYSIPRAAVRFQWFEFLSNHMDAQGRDLSR-----RGLCGAGVAAE 135
QY 127 SLCEFYPLDFARLADVGRAGAEERERGLDCLVKYKSDGKGLYOGFNVSVOGIIL 186
DB 136 AVVVYCPMEYKVKRTHD--QTSSNPKYRGFPFHGRVREIVRQGLKGTVOGLATVLRKGS 193
QY 187 YRAVFGIYDTAKGMLPDPKNTHIYISMMIAQTVTAVALGTSY---PDTVRRMMQOS 242
DB 194 NQAIRFEVMTSLRMNY--OGDNPNKPMNPLITGVFGAVAGAAVSFGNTPLVDYIKTMQGLE 252
QY 243 GRKGTDMYTGTLDCWRKIARDEGKAFPKGAMSNVLR--GMGAFVLYLYDEIKR 296
DB 253 AHR-----YRNLDCGVOLKNEGKAFYKGTVPRLGVNCIDVALVFIYDEYVK 302

RESULT 14

US-08-518-878B-51
Sequence 51, Application US/08518878B
Patent No. 5702902

GENERAL INFORMATION:
APPLICANT: Tartaglia, Louis A.
TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
TITLE OF INVENTION: TREATMENT OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
STREET: 1155 Avenue of the Americas
CITY: New York
STATE: New York
COUNTRY: U.S.A.
ZIP: 10036-2711

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/518,878B
FILING DATE: 23-AUG-1995
CLASSIFICATION: 435

ATTORNEY/AGENT INFORMATION:
NAME: Coruzzi, Laura A.
REGISTRATION NUMBER: 30,742
REFERENCE/DOCKET NUMBER: 7853-036
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 790-9090
TELEFAX: (212) 869-9741/8864

INFORMATION FOR SEQ ID NO: 51:
SEQUENCE CHARACTERISTICS:
LENGTH: 309 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
US-08-518-878B-51

Query Match 15.58; Score 239.5; DB 1; Length 309;
 Best Local Similarity 23.58; Pred. No. 4,4e-19;
 Matches 72; Conservative 58; Mismatches 149; Indels 27; Gaps 8;

2 TDAALSPKDFLAGVAAIASTKTAIVAPIERVKLLIQVHASK---QTADKQKGIIDCV 58
 7 TDVPPATVYKFLAGTRACIADLITPPLDAKVRLOQSGSPVATVSAQIRGVNGTI 66
 59 VRIKQEVLSFWRGNLAVIRYFPQALNFAFKDKYQIFLGVDKRTQFWMYFAGNLA 118
 67 LTVVRTEGPRSLYNGLVAGLQROMSFASVIRIGLYDSVKQFYTKGSEHAS-----ISRL 121
 119 SGGAAGTSLCFYYPPLDFATRLAADYKAGARERGLDCLVKIKSGIGLYOGFN 178
 122 AGSTTGALAVAAQPTDVVVRFOAQ-ARAGGRRQSTVNAYKTTAREGFRGLMKGTS 180
 179 VSVGGIITYRAAYFGIYDTAK-----GMLPDKRNTIIVISMIAQVTVAVAGLTSYF 232
 181 PNVARNATVCAELVYTDLIKDALLRANLMTDLPCHFTSAFGAGCTTYIAS---PVD 236
 233 TVRRRMMS-GRKGTDIMYTGTLDCWRKIARDEGKAFKGAWSNVL-R-GMGAFVYL 290
 237 VVKTRYNSALGO-----YSSAGHCALTMLOKEGPRAFYKGMPSFLRLGSMNVVMFY 290
 291 YDEIKR 296
 291 YEOLKR 296

RESULT 15
 US-08-807-861A-51
 ; Sequence 51, Application US/08807861A
 ; Patent No. 5853975
 ; GENERAL INFORMATION:
 ; APPLICANT: Tartaglia, Louis A.
 ; TITLE OF INVENTION: METHODS AND COMPOSITIONS FOR THE
 ; TITLE OF INVENTION: REGULATION OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
 ; NUMBER OF SEQUENCES: 64
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pennie & Edmonds LLP
 ; STREET: 1155 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: U.S.A.
 ; ZIP: 10036-2711
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patentin Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/807,861A
 ; FILING DATE: 26-FEB-1997
 ; CLASSIFICATION: 514
 ; PRIOR APPLICATION DATA:
 ; APPLICATION NUMBER: US 08/518,878
 ; FILING DATE: 23-AUG-1995
 ; APPLICATION NUMBER: US 08/470,868
 ; FILING DATE: 06-JUN-1995
 ; APPLICATION NUMBER: US 08/294,522
 ; FILING DATE: 23-AUG-1994
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Coruzzi, Laura A.
 ; REGISTRATION NUMBER: 30,742
 ; REFERENCE/DOCKET NUMBER: 7853-066
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (212) 790-9090
 ; TELEFAX: (212) 869-9741/8864
 ; TELEX: 66141 PENNIE
 ; INFORMATION FOR SEQ ID NO: 51:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 309 amino acids
 ; TYPE: amino acid

STRANDEDNESS: single
 TOPOLOGY: unknown
 ; US-08-807-861A-51

Query Match 15.58; Score 239.5; DB 2; Length 309;
 Best Local Similarity 23.58; Pred. No. 4,4e-19;
 Matches 72; Conservative 58; Mismatches 149; Indels 27; Gaps 8;

2 TDAALSPKDFLAGVAAIASTKTAIVAPIERVKLLIQVHASK---QTADKQKGIIDCV 58
 7 TDVPPATVYKFLAGTRACIADLITPPLDAKVRLOQSGSPVATVSAQIRGVNGTI 66
 59 VRIKQEVLSFWRGNLAVIRYFPQALNFAFKDKYQIFLGVDKRTQFWMYFAGNLA 118
 67 LTVVRTEGPRSLYNGLVAGLQROMSFASVIRIGLYDSVKQFYTKGSEHAS-----ISRL 121
 119 SGGAAGTSLCFYYPPLDFATRLAADYKAGARERGLDCLVKIKSGIGLYOGFN 178
 122 AGSTTGALAVAAQPTDVVVRFOAQ-ARAGGRRQSTVNAYKTTAREGFRGLMKGTS 180
 179 VSVGGIITYRAAYFGIYDTAK-----GMLPDKRNTIIVISMIAQVTVAVAGLTSYF 232
 181 PNVARNATVCAELVYTDLIKDALLRANLMTDLPCHFTSAFGAGCTTYIAS---PVD 236
 233 TVRRRMMS-GRKGTDIMYTGTLDCWRKIARDEGKAFKGAWSNVL-R-GMGAFVYL 290
 237 VVKTRYNSALGO-----YSSAGHCALTMLOKEGPRAFYKGMPSFLRLGSMNVVMFY 290
 291 YDEIKR 296
 291 YEOLKR 296

Search completed: August 28, 2003, 19:44:19
 Job time : 19.0202 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 28, 2003, 19:38:56 ; Search time 19.355 Seconds

(without alignments)
2105.969 Million cell updates/sec

Title: US-09-811-132-32

Perfect score: 1547
Sequence: 1 MTDALSPAKDFLAGVAA.....LRGNGAFVLVYDEIKRYT 298

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 510680 seqs, 136781880 residues

Total number of hits satisfying chosen parameters: 510680

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications_AA:*

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2: /cgn2_6/ptodata/1/pubppa/PCr_NEW_PUB.pep:*

3: /cgn2_6/ptodata/1/pubppa/US06_NEW_PUB.pep:*

4: /cgn2_6/ptodata/1/pubppa/US06_PUBCOMB.pep:*

5: /cgn2_6/ptodata/1/pubppa/US07_NEW_PUB.pep:*

6: /cgn2_6/ptodata/1/pubppa/PCrUS_PUBCOMB.pep:*

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9: /cgn2_6/ptodata/1/pubppa/US09_PUBCOMB.pep:*

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11: /cgn2_6/ptodata/1/pubppa/US09C_PUBCOMB.pep:*

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14: /cgn2_6/ptodata/1/pubppa/US10_PUBCOMB.pep:*

15: /cgn2_6/ptodata/1/pubppa/US10C_PUBCOMB.pep:*

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17: /cgn2_6/ptodata/1/pubppa/US60_NEW_PUB.pep:*

18: /cgn2_6/ptodata/1/pubppa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
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| 1 | 1547 | 100.0 | 298 | 9 | US-09-811-094-32 |
| 2 | 1547 | 100.0 | 298 | 9 | US-09-810-644-32 |
| 3 | 1547 | 100.0 | 298 | 10 | US-09-185-904A-32 |
| 4 | 1454 | 94.0 | 298 | 9 | US-09-811-094-33 |
| 5 | 1454 | 94.0 | 298 | 9 | US-09-810-644-33 |
| 6 | 1454 | 94.0 | 298 | 10 | US-09-185-904A-33 |
| 7 | 1391.5 | 89.9 | 297 | 9 | US-09-811-094-31 |
| 8 | 1391.5 | 89.9 | 297 | 9 | US-09-810-644-31 |
| 9 | 1391.5 | 89.9 | 297 | 10 | US-09-185-904A-31 |
| 10 | 752.5 | 48.6 | 318 | 10 | US-09-801-368-252 |
| 11 | 741.5 | 47.9 | 381 | 12 | US-10-141-478A-2 |
| 12 | 741.5 | 47.9 | 386 | 9 | US-09-734-569-170 |
| 13 | 734 | 47.4 | 308 | 15 | US-10-128-714-3338 |
| 14 | 734 | 47.4 | 308 | 15 | US-10-128-714-8338 |
| 15 | 677.5 | 43.8 | 677 | 12 | US-10-259-165-192 |

| | | | | | | |
|----|-------|------|-----|----|---------------------|--------------------|
| 16 | 484 | 31.3 | 132 | 9 | US-09-925-301-1459 | Sequence 1459, App |
| 17 | 448 | 29.0 | 87 | 9 | US-09-864-761-36440 | Sequence 36440, A |
| 18 | 351 | 22.7 | 477 | 10 | US-09-777-921A-2 | Sequence 2, App11 |
| 19 | 350 | 22.6 | 475 | 10 | US-09-777-921A-4 | Sequence 4, App11 |
| 20 | 323.5 | 20.9 | 410 | 10 | US-09-777-921A-5 | Sequence 5, App11 |
| 21 | 302 | 19.5 | 469 | 9 | US-09-989-722-289 | Sequence 289, App |
| 22 | 302 | 19.5 | 469 | 9 | US-09-989-723-289 | Sequence 289, App |
| 23 | 302 | 19.5 | 469 | 9 | US-09-989-279-289 | Sequence 289, App |
| 24 | 302 | 19.5 | 469 | 9 | US-09-989-727-289 | Sequence 289, App |
| 25 | 302 | 19.5 | 469 | 10 | US-09-989-731-289 | Sequence 289, App |
| 26 | 302 | 19.5 | 469 | 10 | US-09-989-732-289 | Sequence 289, App |
| 27 | 302 | 19.5 | 469 | 10 | US-09-981-073-289 | Sequence 289, App |
| 28 | 302 | 19.5 | 469 | 10 | US-09-990-442-289 | Sequence 289, App |
| 29 | 302 | 19.5 | 469 | 10 | US-09-991-163-289 | Sequence 289, App |
| 30 | 302 | 19.5 | 469 | 10 | US-09-993-604-289 | Sequence 289, App |
| 31 | 302 | 19.5 | 469 | 10 | US-09-990-456-289 | Sequence 289, App |
| 32 | 302 | 19.5 | 469 | 10 | US-09-990-444-289 | Sequence 289, App |
| 33 | 302 | 19.5 | 469 | 10 | US-09-992-598-289 | Sequence 289, App |
| 34 | 302 | 19.5 | 469 | 10 | US-09-989-293A-289 | Sequence 289, App |
| 35 | 302 | 19.5 | 469 | 10 | US-09-989-735-289 | Sequence 289, App |
| 36 | 302 | 19.5 | 469 | 10 | US-09-990-444-289 | Sequence 289, App |
| 37 | 302 | 19.5 | 469 | 10 | US-09-991-181-289 | Sequence 289, App |
| 38 | 302 | 19.5 | 469 | 10 | US-09-989-730-289 | Sequence 289, App |
| 39 | 302 | 19.5 | 469 | 10 | US-09-990-436-289 | Sequence 289, App |
| 40 | 302 | 19.5 | 469 | 10 | US-09-993-687-289 | Sequence 289, App |
| 41 | 302 | 19.5 | 469 | 11 | US-09-989-734-289 | Sequence 289, App |
| 42 | 302 | 19.5 | 469 | 11 | US-09-997-653-289 | Sequence 289, App |
| 43 | 302 | 19.5 | 469 | 11 | US-09-993-667-289 | Sequence 289, App |
| 44 | 302 | 19.5 | 469 | 11 | US-09-997-628-289 | Sequence 289, App |
| 45 | 302 | 19.5 | 469 | 11 | US-09-997-666-289 | Sequence 289, App |

ALIGNMENTS

RESULT 1
US-09-811-094-32
; Sequence 32, Application US/09811094
; Patent No. US20010044144A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, Christen M.
; APPLICANT: Davis, Robert E.
; APPLICANT: Clevenger, William
; APPLICANT: Wiley, Sandra Eileen
; APPLICANT: Willet, Scott W.
; APPLICANT: Szabo, Tomas R.
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Moos, Walter H.
; APPLICANT: Pel, Yashong
; TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),
; TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR
; FILE REFERENCE: 660088.420D4
; CURRENT FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 32
; LENGTH: 298
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-811-094-32

Query Match 100.0%; Score 1547; DB 9; Length 298;
Best Local Similarity 100.0%; Pred. No. 4.2e-159;
Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MTDALSPAKDFLAGVAAISKTAADIERVKLLQVHASKOITADKQKGIIDCVR 60
DB 1 MTDALSPAKDFLAGVAAISKTAADIERVKLLQVHASKOITADKQKGIIDCVR 60
QY 61 IPKREVSFPRGNANTIRFPQALNFAFKDKYKQIFLGGVDRKQFPMFVFNGLASG 120
DB 61 IPKREVSFPRGNANTIRFPQALNFAFKDKYKQIFLGGVDRKQFPMFVFNGLASG 120

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OY      121 GAAGTSTLCFYYPDLDFATRLAADYGGKGAEEFPGDCLVYIKSPGICKLYOGFNVS 180
      121 GAGGTSTLCFYYPDLDFATRLAADYGGKGAEEFPGDCLVYIKSPGICKLYOGFNVS 180
Db      121 GAGGTSTLCFYYPDLDFATRLAADYGGKGAEEFPGDCLVYIKSPGICKLYOGFNVS 180
OY      161 VGGIITTYAAAFGIYDTAKGMLPDPKNTNHIYISMMIAOTVTAVAGLTSYFPDVTARRMM 240
      161 VGGIITTYAAAFGIYDTAKGMLPDPKNTNHIYISMMIAOTVTAVAGLTSYFPDVTARRMM 240
Db      161 VGGIITTYAAAFGIYDTAKGMLPDPKNTNHIYISMMIAOTVTAVAGLTSYFPDVTARRMM 240
OY      241 QSGRKGTDIMYTGTLDCWRKIARDEGGAFFFGAMSNNLRGMGAFAVLVLYDEIKKYT 298
      241 QSGRKGTDIMYTGTLDCWRKIARDEGGAFFFGAMSNNLRGMGAFAVLVLYDEIKKYT 298
Db      241 QSGRKGTDIMYTGTLDCWRKIARDEGGAFFFGAMSNNLRGMGAFAVLVLYDEIKKYT 298

RESULT 2
US-09-810-644-32
; Sequence 32, Application US/09810644
; Patent No. US2002012992A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, Christen M.
; APPLICANT: Davis, Robert E.
; APPLICANT: Clevenger, William
; APPLICANT: Wiley, Sandra Eileen
; APPLICANT: Miller, Scott W.
; APPLICANT: Szabo, Tomas R.
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Moos, Walter H.
; APPLICANT: Pel, Vazhong
; TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLATOR (ANT),
; TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR
; FILE REFERENCE: 660088.420D3
; CURRENT APPLICATION NUMBER: US/09/810,644
; CURRENT FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO: 32
; LENGTH: 298
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-810-644-32

Query Match      100.0%; Score 1547; DB 9; Length 298;
Best Local Similarity 100.0%; Pred. No. 4,2e-159;
Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

OY      1 MTDAAISAPKQFLAGVAAAIKSTVADIERVKLLQVQHSKQTTADKOYKGIIDCYVR 60
Db      1 MTDAAISAPKQFLAGVAAAIKSTVADIERVKLLQVQHSKQTTADKOYKGIIDCYVR 60
OY      61 IPKEDEVLSFWRGNLANVIRYPTQALNFAEKDKYQJIFLGVDKRTQFMRYFAGNLASG 120
      61 IPKEDEVLSFWRGNLANVIRYPTQALNFAEKDKYQJIFLGVDKRTQFMRYFAGNLASG 120
Db      61 IPKEDEVLSFWRGNLANVIRYPTQALNFAEKDKYQJIFLGVDKRTQFMRYFAGNLASG 120
OY      121 GAAAGTSTLCFYYPDLDFATRLAADYGGKGAEEFPGDCLVYIKSPGICKLYOGFNVS 180
      121 GAAAGTSTLCFYYPDLDFATRLAADYGGKGAEEFPGDCLVYIKSPGICKLYOGFNVS 180
Db      121 GAAAGTSTLCFYYPDLDFATRLAADYGGKGAEEFPGDCLVYIKSPGICKLYOGFNVS 180
OY      161 VGGIITTYAAAFGIYDTAKGMLPDPKNTNHIYISMMIAOTVTAVAGLTSYFPDVTARRMM 240
      161 VGGIITTYAAAFGIYDTAKGMLPDPKNTNHIYISMMIAOTVTAVAGLTSYFPDVTARRMM 240
Db      161 VGGIITTYAAAFGIYDTAKGMLPDPKNTNHIYISMMIAOTVTAVAGLTSYFPDVTARRMM 240
OY      241 QSGRKGTDIMYTGTLDCWRKIARDEGGAFFFGAMSNNLRGMGAFAVLVLYDEIKKYT 298
      241 QSGRKGTDIMYTGTLDCWRKIARDEGGAFFFGAMSNNLRGMGAFAVLVLYDEIKKYT 298
Db      241 QSGRKGTDIMYTGTLDCWRKIARDEGGAFFFGAMSNNLRGMGAFAVLVLYDEIKKYT 298

RESULT 3
US-09-185-904A-32
; Sequence 32, Application US/09185904A
; Patent No. US20020177185A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, Christen M.
; APPLICANT: Davis, Robert E.

```

```

APPLICANT: Clevengeter, William
APPLICANT: Willey, Sandra Eileen
APPLICANT: Willey, Scott W.
APPLICANT: Szabo, Tomas R.
APPLICANT: Ghosh, Soumitra S.
TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE
TITLE OF INVENTION: TRANSLATOR (ANT), NOVEL ANT LIGANDS AND SCREENING ASSAYS
FILE REFERENCE: 660088.420
CURRENT APPLICATION NUMBER: US/09/185,904A
CURRENT FILING DATE: 1998-11-03
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 32
LENGTH: 298
TYPE: PRT
ORGANISM: Homo sapien
US-09-185-904A-32

Query Match      100.0%; Score 1547; DB 10; Length 298;
Best Local Similarity 100.0%; Pred. No. 4,2e-159;
Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MTDAAISFADFLAGVAAAIKSTAAVAPIERVKLLLOVQASAKITADKQYKGIIDCYR 60
DB      1 MTDAAISFADFLAGVAAAIKSTAAVAPIERVKLLLOVQASAKITADKQYKGIIDCYR 60
QY      61 IPKQEVLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKRTQFRRYFAGNLASG 120
DB      61 IPKQEVLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKRTQFRRYFAGNLASG 120
QY      121 GAAGATSLCYFPYPLDFPARTLADYGAAGAREFRGJGDCLVKTKSDGJIKGLYOGFNVS 180
DB      121 GAAGATSLCYFPYPLDFPARTLADYGAAGAREFRGJGDCLVKTKSDGJIKGLYOGFNVS 180
QY      181 VGGIITRAAVFGLYIDPAKGMPLPPKNTHTYISMIAQTYTAAGLSYFPDQYRRRMM 240
DB      181 VGGIITRAAVFGLYIDPAKGMPLPPKNTHTYISMIAQTYTAAGLSYFPDQYRRRMM 240
QY      241 QSGRKGTDIMYTGTLDCWRKIARDEGSKAFPFKAMSIVNLGMSGAFVLLVYDEIKKYT 298
DB      241 QSGRKGTDIMYTGTLDCWRKIARDEGSKAFPFKAMSIVNLGMSGAFVLLVYDEIKKYT 298

RESULT 4
US-09-811-094-33
Sequence 33, Application US/09811094
Patent No. US2001004414A1
GENERAL INFORMATION:
APPLICANT: Anderson, Christen M.
APPLICANT: Davis, Robert E.
APPLICANT: Clevengeter, William
APPLICANT: Willey, Sandra Eileen
APPLICANT: Willey, Scott W.
APPLICANT: Szabo, Tomas R.
APPLICANT: Ghosh, Soumitra S.
APPLICANT: Moos, Walter H.
APPLICANT: Pei, Yezhong
TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLATOR (ANT),
FILE REFERENCE: 660088.420D4
CURRENT APPLICATION NUMBER: US/09/811,094
CURRENT FILING DATE: 2001-03-14
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FASTSEQ for Windows Version 3.0
SEQ ID NO 33
LENGTH: 298
TYPE: PRT
ORGANISM: Homo sapien
US-09-811-094-33

Query Match      94.0%; Score 1454; DB 9; Length 298;
Best Local Similarity 92.6%; Pred. No. 4,9e-149;

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Matches 274; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

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OY 1 MTDALSFADKDFLAGVAAAIKTAAPIERVKLLQVOHASKOITADKQYKGIIDCYVR 60
  ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MTEQAISPAKDFLAGGIAAISKTAAPIERVKLLQVOHASKOITADKQYKGIIDCYVR 60
OY 61 IPKEQEVLSFWKGNLANIYRFPQALNFAFKDKYKQJFLGVDKRTQFWRYFAGNLSG 120
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 IPKEQEVLSFWKGNLANIYRFPQALNFAFKDKYKQJFLGVDKRTQFWRYFAGNLSG 120
OY 121 GAAGATSLCFYPPDLPFARTRLAADVGKAGAREFERGLDCLVKIKSDGIRGLYOGFSVS 180
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 GAAGATSLCFYPPDLPFARTRLAADVGKAGAREFERGLDCLVKIKSDGIRGLYOGFSVS 180
OY 181 VOGIIYRAAYFGYIDFAKGMLPDPKNTNHIYSMMIAOTVAVAGLTSYPPDTPVRRMM 240
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 181 VOGIIYRAAYFGYIDFAKGMLPDPKNTNHIYSMMIAOTVAVAGVSPDTPVRRMM 240
OY 241 QSGRKGTDIMYTGTLDCWKRKIARDEGKAFKGAAMSVNLKMGAFVLVLYDEIRK 296
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 241 QSGRKGADIMYTGTVDCWKRKIFRDEGKAFKGAAMSVNLKMGAFVLVLYDELK 296
```

RESULT 5

US-09-810-644-33
Sequence 33, Application US/09810644
Patent No. US20020012992A1

GENERAL INFORMATION:

APPLICANT: Anderson, Christen M.
APPLICANT: Davis, Robert E.
APPLICANT: Clevenger, William
APPLICANT: Wiley, Sandra Eileen
APPLICANT: Miller, Scott W.
APPLICANT: Szabo, Tomas R.
APPLICANT: Ghosh, Soumitra S.
APPLICANT: Moos, Walter H.
TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),
TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR
FILE REFERENCE: 660088.420D3
CURRENT APPLICATION NUMBER: US/09/810,644
CURRENT FILING DATE: 2001-03-14
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 33
LENGTH: 298
TYPE: PRT
ORGANISM: Homo sapien
US-09-810-644-33

Query Match 94.0%; Score 1454; DB 9; Length 298;
Best Local Similarity 92.6%; Pred. No. 4.9e-149;
Matches 274; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

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OY 1 MTDALSFADKDFLAGVAAAIKTAAPIERVKLLQVOHASKOITADKQYKGIIDCYVR 60
  ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MTEQAISPAKDFLAGGIAAISKTAAPIERVKLLQVOHASKOITADKQYKGIIDCYVR 60
OY 61 IPKEQEVLSFWKGNLANIYRFPQALNFAFKDKYKQJFLGVDKRTQFWRYFAGNLSG 120
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 IPKEQEVLSFWKGNLANIYRFPQALNFAFKDKYKQJFLGVDKRTQFWRYFAGNLSG 120
OY 121 GAAGATSLCFYPPDLPFARTRLAADVGKAGAREFERGLDCLVKIKSDGIRGLYOGFSVS 180
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 GAAGATSLCFYPPDLPFARTRLAADVGKAGAREFERGLDCLVKIKSDGIRGLYOGFSVS 180
OY 181 VOGIIYRAAYFGYIDFAKGMLPDPKNTNHIYSMMIAOTVAVAGLTSYPPDTPVRRMM 240
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 181 VOGIIYRAAYFGYIDFAKGMLPDPKNTNHIYSMMIAOTVAVAGVSPDTPVRRMM 240
OY 241 QSGRKGTDIMYTGTLDCWKRKIARDEGKAFKGAAMSVNLKMGAFVLVLYDEIRK 296
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 241 QSGRKGADIMYTGTVDCWKRKIFRDEGKAFKGAAMSVNLKMGAFVLVLYDELK 296
```

RESULT 6

US-09-185-904A-33
Sequence 33, Application US/09185904A
Patent No. US20020177185A1

GENERAL INFORMATION:

APPLICANT: Anderson, Christen M.
APPLICANT: Davis, Robert E.
APPLICANT: Clevenger, William
APPLICANT: Wiley, Sandra Eileen
APPLICANT: Miller, Scott W.
APPLICANT: Szabo, Tomas R.
APPLICANT: Ghosh, Soumitra S.
TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE
TITLE OF INVENTION: TRANSLOCATOR (ANT), NOVEL ANT LIGANDS AND SCREENING ASSAYS
FILE REFERENCE: 660088.420
CURRENT APPLICATION NUMBER: US/09/185,904A
CURRENT FILING DATE: 1998-11-03
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 33
LENGTH: 298
TYPE: PRT
ORGANISM: Homo sapien
US-09-185-904A-33

Query Match 94.0%; Score 1454; DB 10; Length 298;
Best Local Similarity 92.6%; Pred. No. 4.9e-149;
Matches 274; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

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OY 1 MTDALSFADKDFLAGVAAAIKTAAPIERVKLLQVOHASKOITADKQYKGIIDCYVR 60
  ||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 1 MTEQAISPAKDFLAGGIAAISKTAAPIERVKLLQVOHASKOITADKQYKGIIDCYVR 60
OY 61 IPKEQEVLSFWKGNLANIYRFPQALNFAFKDKYKQJFLGVDKRTQFWRYFAGNLSG 120
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 61 IPKEQEVLSFWKGNLANIYRFPQALNFAFKDKYKQJFLGVDKRTQFWRYFAGNLSG 120
OY 121 GAAGATSLCFYPPDLPFARTRLAADVGKAGAREFERGLDCLVKIKSDGIRGLYOGFSVS 180
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 121 GAAGATSLCFYPPDLPFARTRLAADVGKAGAREFERGLDCLVKIKSDGIRGLYOGFSVS 180
OY 181 VOGIIYRAAYFGYIDFAKGMLPDPKNTNHIYSMMIAOTVAVAGLTSYPPDTPVRRMM 240
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 181 VOGIIYRAAYFGYIDFAKGMLPDPKNTNHIYSMMIAOTVAVAGVSPDTPVRRMM 240
OY 241 QSGRKGTDIMYTGTLDCWKRKIARDEGKAFKGAAMSVNLKMGAFVLVLYDEIRK 296
  |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db 241 QSGRKGADIMYTGTVDCWKRKIFRDEGKAFKGAAMSVNLKMGAFVLVLYDELK 296
```

RESULT 7

US-09-811-094-31
Sequence 31, Application US/09811094
Patent No. US2001004414A1

GENERAL INFORMATION:

APPLICANT: Anderson, Christen M.
APPLICANT: Davis, Robert E.
APPLICANT: Clevenger, William
APPLICANT: Wiley, Sandra Eileen
APPLICANT: Miller, Scott W.
APPLICANT: Szabo, Tomas R.
APPLICANT: Ghosh, Soumitra S.
APPLICANT: Moos, Walter H.
TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),
TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR
FILE REFERENCE: 660088.420D4
CURRENT APPLICATION NUMBER: US/09/811,094
CURRENT FILING DATE: 2001-03-14
NUMBER OF SEQ ID NOS: 37

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: SOFTWARE: fastseq for Windows Version 3.0
: SEQ ID NO 31
: LENGTH: 297
: TYPE: prt
: ORGANISM: Homo sapien
US-09-811-094-31

```

| | | | | |
|-----------------------|-----------------|--------------------|----------|------------|
| Query Match | 89.9% | Score 1391.5 | DB 9 | Length 297 |
| Best Local Similarity | 88.6% | Prod. No. 2.9e-142 | | |
| Matches 263 | Conservative 17 | Mismatches 16 | Indels 1 | Gaps 1 |

QY 1 MDAALASPFKADFLAGGVAALISKTVAAIERKLLLYQVHASKQITADKKYKGLTDCVVR 60
 QY 1 MGHAMSFLLKDFLAGVAAVASKTAAVIERKLLLYQVHASQISAKQYKGLTDCVVR 60
 Db 1
 QY 61 IPEQEVLSFMRGNLANVIRYPTQALNPAERKKYKQILGCVDKRPIQWFRYFAGNLASG 120
 Db 61 IPEQEVLSFMRGNLANVIRYPTQALNPAERKKYKQILGCVDRHQQFMRKYFAGNLASG 120
 QY 121 GAAGATSLCFVYPLDPARTRLAADVGAAGAEREFRGLDCCVYKTKYSKDGTKGLYQGFNV 180
 Db 121 GAAGATSLCFVYPLDPARTRLAADVGR - AQREHFGLEDCCITKTKFSKDGTLGGLYQGFNV 179
 QY 181 VGGIITRYAAFYGILYDTAKGMLPDBKNTHIYISWMLAQTVTAVALGTSYEPDTVRRMM 240
 Db 180 VGGIITRYAAFYGVYDTAKGMLPDBKNTHIFVSWMLAQSVTAVALGTSYEPDTVRRMM 239
 QY 241 QSRKKTDMYTGTLDCWRKTIARDEGKAFRKGASNTLRMGAGFVLVLYLDEKKY 237
 Db 240 QSRKKTDMYTGTLDCWRKTIARDEGKAFRKGASNTLRMGAGFVLVLYLDEKKY 236

RESULT 8
US-09-810-644-31
; Sequence 31, Application US/09810644
; Patent No. US20020012992A1

```

1  APPLICANT: Anderson, Christen M.
2  APPLICANT: Davis, Robert E.
3  APPLICANT: Clevenger, William
4  APPLICANT: Wiley, Sandra Eileen
5  APPLICANT: Weller, Scott W.
6  APPLICANT: Szabo, Tomas R.
7  APPLICANT: Ghosh, Soumitra S.
8  APPLICANT: Moos, Walter H.
9  APPLICANT: Bel, Yezhong
10 TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT)
11 TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR
12 FILE REFERENCE: 660088.420D3
13 CURRENT APPLICATION NUMBER: US/09/810,644
14 CURRENT FILING DATE: 2001-03-14
15 NUMBER OF SEQ ID NOS: 37
16 SOFTWARE: FastSeq for Windows Version 3.0
17 SEQ ID NO 31
18 LENGTH: 297
19 TYPE: PRF
20 ORGANISM: Homo sapien
21 IS-09-810-644-31

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[illegible]

| Db | 12 | GAGGATSLCEVYPDPEAFRLAADVGR - AQEEFHGLGDCIIKIFKSDGLRGLYQGENVS | 179 |
|----|-----|--|-----|
| Db | 181 | VGGIIITYRAAYGIVDTAKGMLPDDRKNHIYISMMIAOTYAVAGVLSYEPDPIRRMM | 240 |
| Db | 180 | VGGIIITYRAAYGIVDTAKGMLPDDRKNHIIFSMIAQSYAVAGVLSYEPDIYRRMM | 239 |
| Qy | 241 | QSGRKTDMYTGTLDDQWRKIRADGGGAFPGMANSYLRMGCAFVLYLDEKKY | 237 |
| Qy | 240 | QSGRKADIMTIGTYDDCKRKLIRADGCAKAFEGMANSYLRMGCAFVLYLDEKKI | 236 |

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RESULT 9
US-09-185-904A-31
Sequence 31, Application US/09185904A
Patent No. US2002017185A1
GENERAL INFORMATION:
APPLICANT: Anderson, Christen M.
APPLICANT: Davis, Robert E.
APPLICANT: Clevenger, William
APPLICANT: Wiley, Sandra Eileen
APPLICANT: Miller, Scott W.
APPLICANT: Szabo, Tomas R.
APPLICANT: Ghosh, Soumitra S.
TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE
TITLE OF INVENTION: TRANSLOCATOR (ANT), NOVEL ANT LIGANDS AND SCREENING ASSAYS
FILE REFERENCE: 660088.420
CURRENT APPLICATION NUMBER: US/09/185,904A
CURRENT FILING DATE: 1998-11-03
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 31
LENGTH: 297
TYPE: PRT
ORGANISM: Homo sapien
US-09-185-904A-31

```

| | | | | |
|-----------------------|-----------------|--|----------|------------|
| Query Match | 89.9% | Score 1391.5 | DB 10 | Length 297 |
| Best Local Similarity | 88.6% | Pred. No. 2.9e-142 | | |
| Matches 263 | Conservative 17 | Mismatches 16 | Indels 1 | Gaps 1 |
| QY | 1 | MTDAALSPAKDFLGGVAAAISKTAVADIERVKLLLOVHASKOITADKOYKGIIDCVRR | 60 | |
| Db | 1 | MGDAWMSLTKPLFGLAGVAAAASKTAVADIERVKLLLOVHASKOISAKOYKGIIDCVRR | 60 | |
| QY | 61 | IPKHOEVLSEPMRGNLANVIRYEPFOALNFAFADKKOIFLGVDKRRQPFWRFAENLNSG | 120 | |
| Db | 61 | IPKHOGLSEPMRGNLANVIRYEPFOALNFAFADKKOIFLGVDKRRQPFWRFAENLNSG | 120 | |
| QY | 121 | GAAGATSLCFEYPLDFPARRLADVDGKAGAEERERFGLDCLVYIKKSDGIKGLYOGFNVS | 180 | |
| Db | 121 | GAAGATSLCFEYPLDFPARRLADVDGRR-AQREFHGLDCLCIKIPKSGRLRLOXGFNVS | 179 | |
| QY | 181 | VGGIITIRAAAFGYLDITAKGLPDPKKNHIYISMMIAOTVAVAGLTSYFEDTVRRRMM | 240 | |
| Db | 180 | VGGIITIRAAAFGYLDITAKGLPDPKKNHIYISMMIAOSVTAVAGLTSYFEDTVRRRMM | 239 | |
| QY | 241 | QSGRRKGDIMYTGGLDCKRTARDEGCAAFKRGAMSNVLRMGCAFVLYLDEIKY | 297 | |
| Db | 240 | QSGRRKGDIMYTGVDCKRTAKDEGAFAFKGAMSNVLRMGCAFVLYLDEIKY | 296 | |

RESULT 10
US-09-801-368-252
Sequence 252, Application US/09801368
Patent No. US20020128250A1
GENERAL INFORMATION:
APPLICANT: Busby, Robert
APPLICANT: Call, Brian
APPLICANT: Hecht, Peter
APPLICANT: Holtzman, Doug
APPLICANT: Madden, Kevin
APPLICANT: Maxon, Mary

RESULT 10
US-09-801-368-252
Sentence 252, APPENDIX US/09801368
: Patent No. US20020128250A1
: GENERAL INFORMATION:
: :
: APPLICANT: Busby, Robert
: APPLICANT: Call, Brian
: APPLICANT: Hecht, Peter
: APPLICANT: Holtzman, Doug
: APPLICANT: Madden, Kevin
: APPLICANT: Maxon, Mary

APPLICANT: Moughamer, Todd
APPLICANT: Provart, Nicholas
APPLICANT: Rieke, Darrell
TITLE OF INVENTION: GENES THAT ARE MODULATED BY POSTTRANSCRIPTIONAL GENE SILENCING
FILE REFERENCE: 70030-NP
CURRENT APPLICATION NUMBER: US/10/259,165
CURRENT FILING DATE: 2002-09-26
PRIOR APPLICATION NUMBER: US 60/370,620
PRIOR FILING DATE: 2002-04-04
PRIOR APPLICATION NUMBER: US 60/368,327
PRIOR FILING DATE: 2002-03-27
PRIOR APPLICATION NUMBER: US 60/325,277
PRIOR FILING DATE: 2001-09-26
NUMBER OF SEQ ID NOS: 782
SOFTWARE: Patentlist.pl version 3.0.4 (C) 2001 Syngenta
SEQ ID NO 192
LENGTH: 677
TYPE: PRT
ORGANISM: Oryza sativa
US-10-259-165-192

Query Match 43.8%; Score 677.5; DB 12; Length 677;

Best Local Similarity 50.5%; Pred. No. 1.9e-64;

Matches 154; Conservative 39; Mismatches 89; Indels 23; Gaps 8;

OY 8 FAKDFLAGVAATAISKTAVAPIERVKLLQVO-HASKQITADKQYKGLIDCVIRIPKEQE 66
DB 376 FMIDPMGVSAAVSKTAAPIERIKLQNDDEMIKGRLSHPKGIADCEGRIRKDEG 435
OY 67 VLSTFRGLANVIRYEPQALNFAFKDKYKQIFLAGVDKRTQFWRYPAGNLASGAGAT 126
DB 436 VIALMRGNTANVIRYEPQALNFAFKDKHFKMFNFKKDK-DGYWKMFAGNLASGAGAGAC 494
OY 127 SLCEFYPLDFARTLAD--VGKAGAREFRGLGDCLVKIKYKSDGIRKGLYGF-NVSYQG 183
DB 495 SLFEVYSLDYARTLANDAKAAKGGKQFNGLDVYRKTLASDSIAGLPIQLPVLV 554
OY 184 IITRAAYFGIYDPAK---GMLPDPKNTTHIVISMTAQVTAVAGLTSYPPEDTVRRRM 238
DB 555 SLNNGLYFGMYDSLKPVVGNLQD---NFLASFLGWTITGAGLASYPIDTVRRRM 610
OY 239 MMOSGRKGTDMYTGTLDCMKRIARDEGKAFPKGAMSNVLRGMGAFVLVLYDEI---- 294
DB 611 MMTSGEA---VKYNSLDAFKQIVAKEGAKSLFKGAGANILRAVAGVLAGYDKLQVVV 667
OY 295 --KKY 297
DB 668 FGKKY 672

Search completed: August 28, 2003, 19:45:24
Job time : 20.355 secs

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OM protein - protein search, using sw model

Run on: August 28, 2003, 19:35:01 ; Search time 20.6898 Seconds

(without alignments)
1385.139 Million cell updates/sec

Title: US-09-811-132-32

Perfect score: 1347

Sequence: 1 MTDAISFAKDFLAGVAA.....LRGMCARVLYDEIKRYT 298

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 283308 segs, 9616862 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Database : PIR_76:*

1: p1r1:*

2: p1r2:*

3: p1r3:*

4: p1r4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|----------|---------------------|
| 1 | 1547 | 100.0 | 298 | 1 A29132 | ADP, ATP carrier pr |
| 2 | 1479 | 95.6 | 298 | 2 S31814 | ADP, ATP carrier pr |
| 3 | 1458 | 94.2 | 298 | 2 B43646 | ADP, ATP carrier pr |
| 4 | 1454 | 94.0 | 298 | 1 S03894 | ADP, ATP carrier pr |
| 5 | 1419 | 91.7 | 298 | 1 XWBO | ADP, ATP carrier pr |
| 6 | 1417 | 91.6 | 298 | 2 S37210 | ADP, ATP carrier pr |
| 7 | 1417 | 91.6 | 298 | 2 S37210 | ADP, ATP carrier pr |
| 8 | 1413 | 91.3 | 298 | 1 A44778 | adenine nucleotide |
| 9 | 1170 | 75.6 | 301 | 1 S31935 | ADP, ATP carrier pr |
| 10 | 1032 | 66.7 | 300 | 2 T25371 | hypothetical prote |
| 11 | 1029 | 66.5 | 313 | 2 T23207 | hypothetical prote |
| 12 | 1029 | 66.5 | 313 | 2 T23207 | hypothetical prote |
| 13 | 986 | 63.7 | 300 | 2 T15206 | hypothetical prote |
| 14 | 968 | 62.6 | 339 | 2 A41677 | ADP, ATP carrier pr |
| 15 | 938 | 60.6 | 301 | 2 S51132 | ADP, ATP carrier pr |
| 16 | 771 | 49.8 | 386 | 2 T08709 | ADP, ATP carrier pr |
| 17 | 770 | 49.8 | 322 | 2 T40526 | ADP, ATP carrier pr |
| 18 | 765 | 49.5 | 308 | 1 S30259 | ADP, ATP carrier pr |
| 19 | 761.5 | 49.2 | 307 | 2 A36582 | ADP, ATP carrier pr |
| 20 | 759 | 49.1 | 326 | 2 T25728 | hypothetical prote |
| 21 | 759 | 49.1 | 387 | 2 S14876 | ADP, ATP carrier pr |
| 22 | 757 | 48.9 | 313 | 1 XWNG | ADP, ATP carrier pr |
| 23 | 754 | 48.7 | 386 | 2 S17917 | ADP, ATP carrier pr |
| 24 | 753 | 48.7 | 387 | 2 S16568 | ADP, ATP carrier pr |
| 25 | 752.5 | 48.6 | 318 | 1 A31978 | ADP, ATP carrier pr |
| 26 | 752 | 48.6 | 386 | 2 S21974 | ADP, ATP carrier pr |
| 27 | 749.5 | 48.4 | 305 | 2 S68154 | ADP, ATP carrier pr |
| 28 | 749.5 | 48.4 | 306 | 2 T20012 | hypothetical prote |
| 29 | 746 | 48.2 | 306 | 2 T42011 | ADP, ATP carrier pr |

| | | | | | |
|----|-------|------|-----|----------|---------------------|
| 30 | 746 | 48.2 | 379 | 2 T04608 | ADP, ATP carrier pr |
| 31 | 745.5 | 48.2 | 385 | 1 S29852 | ADP, ATP carrier pr |
| 32 | 745 | 48.2 | 382 | 2 S33630 | ADP, ATP carrier pr |
| 33 | 741.5 | 47.9 | 379 | 2 S21313 | ADP, ATP carrier pr |
| 34 | 741.5 | 47.9 | 386 | 2 S14874 | ADP, ATP carrier pr |
| 35 | 728 | 47.1 | 309 | 2 A24849 | ADP, ATP carrier pr |
| 36 | 665.5 | 43.0 | 298 | 2 T24029 | ADP, ATP carrier pr |
| 37 | 521.5 | 33.7 | 327 | 2 T51577 | ADP, ATP carrier pr |
| 38 | 388 | 25.1 | 325 | 2 T04273 | hypothetical prote |
| 39 | 372 | 24.0 | 381 | 2 T51158 | hypothetical prote |
| 40 | 372 | 24.0 | 415 | 2 T48171 | hypothetical prote |
| 41 | 356 | 23.0 | 352 | 2 T01729 | hypothetical prote |
| 42 | 350 | 22.6 | 475 | 2 T50686 | peroxisomal Ca-dep |
| 43 | 340 | 22.0 | 358 | 2 T45934 | hypothetical prote |
| 44 | 334 | 21.6 | 348 | 2 D84798 | probable mitochond |
| 45 | 322.5 | 20.8 | 332 | 2 T47703 | Ca-dependent solut |

ALIGNMENTS

RESULT 1

A29132 ADP, ATP carrier protein T2 - human

N:Alternate names: mitochondrial ADP, ATP translocase 2

C:Species: Homo sapiens (man)

C>Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 17-Mar-2000

C:Accession: A29132; C28116

R:Battni, R.; Ferrari, S.; Kaczmarek, L.; Calabretta, B.; Chen, S.; Baserga, R.

J. Biol. Chem. 262, 4355-4359, 1987

A:Title: Molecular cloning of a cDNA for a human ADP/ATP carrier which is growth-regu

A:Reference number: A29132; MID:87166056; PMID:3031073

A:Accession: A29132

A:Molecule type: mRNA

A:Residues: 1-298 <BAT>

A:Cross-references: GB:J03683; NID:q179246; PIDN:AAA3579.1; PID:q179247

R:Houldsworth, J.; Altardi, G.

Proc. Natl. Acad. Sci. U.S.A. 85, 377-381, 1988

A:Title: Two distinct genes for ADP/ATP translocase are expressed at the mRNA level 1

A:Reference number: A94197; MID:88124845; PMID:2829183

A:Accession: C28116

A:Molecule type: mRNA

A:Residues: 47-65, 'G', 67-110, 'L', 112-161, 'G', 163-298 <HOU>

A:Cross-references: GB:J03591; NID:q339720; PIDN:AAA36749.1; PID:q339721

A:Experimental source: clone PHAT3

C:Genetics:

A:Gene: GDB:ANT2; T3; 2F1

A:Cross-references: GDB:125190; OMIM:300150

A:Map position: Xq13-Xq26

A>Note: there may be some confusion in the assignment of sequences for GDB:ANT2 and G

C:Superfamily: ADP, ATP carrier protein; ADP, ATP carrier protein repeat homology

C:Keywords: duplication; homodimer; mitochondrion; transmembrane protein

F:5-99/Domain: ADP, ATP carrier protein repeat homology <ACP>

F:110-202/Domain: ADP, ATP carrier protein repeat homology <ACP>

F:207-298/Domain: ADP, ATP carrier protein repeat homology <ACP>

Query Match 100.0%; Score 1547; DB 1; Length 298;

Best local similarity 100.0%; Pred. No. 4e-130;

Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

| | | | | | |
|----|-----|---|-----|---------------------------------------|----|
| QY | 1 | MTDAISFAKDFLAGVAA | 1 | ISKTAVAPIERVKLLQVHASKQITADKQYGIIDCVVR | 60 |
| DB | 1 | MTDAISFAKDFLAGVAA | 1 | ISKTAVAPIERVKLLQVHASKQITADKQYGIIDCVVR | 60 |
| QY | 61 | IKPEDEVLSFWNGNLANVIRPPTQALNFAFDKVIQITFLGVDKRTQWRFPAGMLASG | 120 | | |
| DB | 61 | IKPEDEVLSFWNGNLANVIRPPTQALNFAFDKVIQITFLGVDKRTQWRFPAGMLASG | 120 | | |
| QY | 121 | GAAGATSLCFVYPLDPAFRLADVGKAGAEFRFGLGCLVITYSDSIRKGYGFNV | 180 | | |
| DB | 121 | GAAGATSLCFVYPLDPAFRLADVGKAGAEFRFGLGCLVITYSDSIRKGYGFNV | 180 | | |
| QY | 181 | VOGIIYRAAYFGIYDTAKGMLPDPKNTIIVISWMIQTAVAVAGITSTYFPDITVRMM | 240 | | |

Db 181 VGGIIRAAVFGIYDTAKGMLPDPKNTHTIVSMIAQVTAVAGLTSTPEDFVRRMM 240
 241 OSGRKGTIDIMVTGLDCWKRIARDEGKAFFKGMNVLMGGAFLVLYDEIKKTT 298
 Db 241 OSGRKGTIDIMVTGLDCWKRIARDEGKAFFKGMNVLMGGAFLVLYDEIKKTT 298

RESULT 2

ADP, ATP carrier protein T2 - mouse
 S31814
 N:Alternate names: adenine nucleotide translocase
 C:Species: Mus musculus (house mouse)
 C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 09-Apr-1998
 C:Accession: S31814
 R:Costel, P.; Laplace, C.
 Submitted to the EMBL Data Library, January 1993
 A:Reference number: S31814
 A:Accession: S31814
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-298 <COS>
 A:Cross-references: EMBL:X70847
 C:Superfamily: ADP, ATP carrier protein; ADP, ATP carrier protein repeat homology
 C:Keywords: duplication; transmembrane protein
 F:5-99/Domain: ADP, ATP carrier protein repeat homology <ACPI>
 F:110-202/Domain: ADP, ATP carrier protein repeat homology <ACP>
 F:207-298/Domain: ADP, ATP carrier protein repeat homology <ACP3>

Query Match 95.68; Score 1479; DB 2; Length 298;
 Best Local Similarity 95.68; Pred. No. 4; Se-124;
 Matches 285; Conservative 4; Mismatches 9; Indels 0; Gaps 0;

QY 1 MTDAAISFANDFLAGVAAAIKSTAVAPIERVKLLQVHASKOITADKOYKGIIDCV 60
 1 MTDAAISFANDFLAGVAAAIKSTAVAPIERVKLLQVHASKOITADKOYKGIIDCV 60
 Db 1 MTDAAISFANDFLAGVAAAIKSTAVAPIERVKLLQVHASKOITADKOYKGIIDCV 60
 QY 61 IPKQEVLSFWRGNLANVIRFPQALNFAFKDKYKQIFLGVDKRFQFRRYRAGNIASG 120
 61 IPKQEVLSFWRGNLANVIRFPQALNFAFKDKYKQIFLGVDKRFQFRRYRAGNIASG 120
 Db 61 IPKQEVLSFWRGNLANVIRFPQALNFAFKDKYKQIFLGVDKRFQFRRYRAGNIASG 120
 QY 121 GAAGATSLCFVYPDPDFARTRIADAVGKAGEREFRGIDCLVTKYKSDGKIGLYOGFNVS 180
 121 GAAGATSLCFVYPDPDFARTRIADAVGKAGEREFRGIDCLVTKYKSDGKIGLYOGFNVS 180
 Db 121 GAAGATSLCFVYPDPDFARTRIADAVGKAGEREFRGIDCLVTKYKSDGKIGLYOGFNVS 180
 QY 181 VGGIIRAAVFGIYDTAKGMLPDPKNTHTIVSMIAQVTAVAGLTSTPEDFVRRMM 240
 181 VGGIIRAAVFGIYDTAKGMLPDPKNTHTIVSMIAQVTAVAGLTSTPEDFVRRMM 240
 Db 181 VGGIIRAAVFGIYDTAKGMLPDPKNTHTIVSMIAQVTAVAGLTSTPEDFVRRMM 240
 QY 241 OSGRKGTIDIMVTGLDCWKRIARDEGKAFFKGMNVLMGGAFLVLYDEIKKTT 298
 241 OSGRKGTIDIMVTGLDCWKRIARDEGKAFFKGMNVLMGGAFLVLYDEIKKTT 298
 Db 241 OSGRKGTIDIMVTGLDCWKRIARDEGKAFFKGMNVLMGGAFLVLYDEIKKTT 298

RESULT 3

ADP, ATP carrier protein T2 - bovine
 B43646
 C:Species: Bos primigenius taurus (cattle)
 C>Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 20-Aug-1999
 C:Accession: B43646
 R:Powell, S.J.; Medd, S.M.; Runswick, M.J.; Walker, J.E.
 A:Title: Two bovine genes for mitochondrial ADP/ATP translocase expressed differently in
 A:Reference number: A43646; MUID:89229093; PMID:2540808
 A:Accession: B43646
 A:Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-298 <POW>
 A:Cross-references: GB:M24103; NID:9529416; PIDN:AAA30769.1; PID:9529417
 C:Superfamily: ADP, ATP carrier protein; ADP, ATP carrier protein repeat homology
 C:Keywords: duplication; homodimer; mitochondrion; transmembrane protein
 F:5-99/Domain: ADP, ATP carrier protein repeat homology <ACPI>
 F:110-202/Domain: ADP, ATP carrier protein repeat homology <ACP>

F:207-298/Domain: ADP, ATP carrier protein repeat homology <ACP3>

Query Match 94.28; Score 1458; DB 2; Length 298;

Best Local Similarity 92.98; Pred. No. 3; Se-122;
 Matches 275; Conservative 13; Mismatches 8; Indels 0; Gaps 0;

QY 1 MTDAAISFANDFLAGVAAAIKSTAVAPIERVKLLQVHASKOITADKOYKGIIDCV 60
 1 MTDAAISFANDFLAGVAAAIKSTAVAPIERVKLLQVHASKOITADKOYKGIIDCV 60
 Db 1 MTDAAISFANDFLAGVAAAIKSTAVAPIERVKLLQVHASKOITADKOYKGIIDCV 60
 QY 61 IPKQEVLSFWRGNLANVIRFPQALNFAFKDKYKQIFLGVDKRFQFRRYRAGNIASG 120
 61 IPKQEVLSFWRGNLANVIRFPQALNFAFKDKYKQIFLGVDKRFQFRRYRAGNIASG 120
 Db 61 IPKQEVLSFWRGNLANVIRFPQALNFAFKDKYKQIFLGVDKRFQFRRYRAGNIASG 120
 QY 121 GAAGATSLCFVYPDPDFARTRIADAVGKAGEREFRGIDCLVTKYKSDGKIGLYOGFNVS 180
 121 GAAGATSLCFVYPDPDFARTRIADAVGKAGEREFRGIDCLVTKYKSDGKIGLYOGFNVS 180
 Db 121 GAAGATSLCFVYPDPDFARTRIADAVGKAGEREFRGIDCLVTKYKSDGKIGLYOGFNVS 180
 QY 181 VGGIIRAAVFGIYDTAKGMLPDPKNTHTIVSMIAQVTAVAGLTSTPEDFVRRMM 240
 181 VGGIIRAAVFGIYDTAKGMLPDPKNTHTIVSMIAQVTAVAGLTSTPEDFVRRMM 240
 Db 181 VGGIIRAAVFGIYDTAKGMLPDPKNTHTIVSMIAQVTAVAGLTSTPEDFVRRMM 240
 QY 241 OSGRKGTIDIMVTGLDCWKRIARDEGKAFFKGMNVLMGGAFLVLYDEIKKTT 296
 241 OSGRKGTIDIMVTGLDCWKRIARDEGKAFFKGMNVLMGGAFLVLYDEIKKTT 296
 Db 241 OSGRKGTIDIMVTGLDCWKRIARDEGKAFFKGMNVLMGGAFLVLYDEIKKTT 296

RESULT 4

ADP, ATP carrier protein T3 - human
 S03894

N:Alternate names: ADP, ATP carrier protein T2 (misidentification); mitochondrial ADP,
 C:Species: Homo sapiens (man)
 C>Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 17-Mar-2000
 C:Accession: S03894; B28116
 R:Cozens, A.L.; Runswick, M.J.; Walker, J.E.

A:Title: DNA sequences of two expressed nuclear genes for human mitochondrial ADP/ATP
 A:Reference number: S03893; MUID:89226396; PMID:2541251
 A:Accession: S03894
 A:Status: not compared with conceptual translation

A:Molecule type: DNA
 A:Residues: 1-298 <CO2>
 R:Houldsworth, J.; Attardi, G.
 Proc. Natl. Acad. Sci. U.S.A. 85, 377-381, 1988
 A:Title: Two distinct genes for ADP/ATP translocase are expressed at the mRNA level 1
 A:Reference number: A94197; MUID:88124845; PMID:2829183
 A:Accession: B28116
 A:Molecule type: mRNA

A:Residues: 36-104, 'R', 106, 'A', 109-298 <HOD>
 A:Cross-references: GB:U03592; NID:9339722; PIDN:AAA36750.1; PID:9339723
 A:Experimental source: liver
 C:Genetics:
 A:Gene: GDB:ANT3; ANT3Y
 A:Cross-references: GDB:125184; OMIM:300151; OMIM:403000
 A:Map position: XP22.32-XP22.32; YP11.3-YP11.3
 A:Note: There may be some confusion in the assignment of sequences for GDB:ANT2 and G
 C:Superfamily: ADP, ATP carrier protein; ADP, ATP carrier protein repeat homology
 C:Keywords: duplication; homodimer; mitochondrion; transmembrane protein
 F:2-298/Product: ADP, ATP carrier protein #status predicted <ANT>
 F:5-99/Domain: ADP, ATP carrier protein repeat homology <ACPI>
 F:110-202/Domain: ADP, ATP carrier protein repeat homology <ACP2>
 F:207-298/Domain: ADP, ATP carrier protein repeat homology <ACP3>

Query Match 94.08; Score 1454; DB 1; Length 298;

Best Local Similarity 92.68; Pred. No. 7; Se-122;
 Matches 274; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

QY 1 MTDAAISFANDFLAGVAAAIKSTAVAPIERVKLLQVHASKOITADKOYKGIIDCV 60
 1 MTDAAISFANDFLAGVAAAIKSTAVAPIERVKLLQVHASKOITADKOYKGIIDCV 60
 Db 1 MTDAAISFANDFLAGVAAAIKSTAVAPIERVKLLQVHASKOITADKOYKGIIDCV 60
 QY 61 IPKQEVLSFWRGNLANVIRFPQALNFAFKDKYKQIFLGVDKRFQFRRYRAGNIASG 120
 61 IPKQEVLSFWRGNLANVIRFPQALNFAFKDKYKQIFLGVDKRFQFRRYRAGNIASG 120
 Db 61 IPKQEVLSFWRGNLANVIRFPQALNFAFKDKYKQIFLGVDKRFQFRRYRAGNIASG 120

Db 61 IPKRGVLSFWRGNLANVIRFPFOALNFAKDKYKQIFLGVDKHNQFMFRFAGNLASG 120
 Qy 121 GAAGATSLCFEYPLDFAFTRLADVGKAGAEERFGLDCLVKIKYSDGKGLYOGFNV 180
 Db 121 GAAGATSLCFEYPLDFAFTRLADVGKSGTEREFGLDCLVKIKYSDGKGLYOGFNV 180
 Qy 181 VGGIITIRAAVFGIYDTAKGMLPDPKNTNHYISWMIAGTVAVAGLSTPPDYARRMM 240
 Db 181 VGGIITIRAAVFGIYDTAKGMLPDPKNTNHYISWMIAGTVAVAGLSTPPDYARRMM 240
 Qy 241 OSGRKGTIDIMTYGTLDCWRKTLARDEGKAFKFGAMSNVLRMGCAFVLVLDKTK 296
 Db 241 OSGRKGTIDIMTYGTLDCWRKTLARDEGKAFKFGAMSNVLRMGCAFVLVLDKTK 296

RESULT 5

XMB0

ADP, ATP carrier protein T1 - bovine
 N:Alternate names: ADP/ATP translocase T1
 C:Species: Bos primigenius taurus (cattle)
 C:Date: 14-Nov-1993 #sequence_revision 22-Jul-1994 #text_change 22-Jun-1999
 C:Accession: A43646; A24822; A03181; A61343; S69369
 R:Powell, S.J.; Medd, S.M.; Runswick, M.J.; Walker, J.E.
 Biochemistry 28, 866-873, 1989
 A:Title: Two bovine genes for mitochondrial ADP/ATP translocase expressed differently in
 A:Reference number: A43646; MUID:89229093; PMID:2540808
 A:Accession: A43646
 A:Residues: 1-298 <POW>
 A:Molecule type: mRNA
 A:Cross-references: GB:M4102; NID:g529414; PIDN:AAA30768.1; PID:g529415
 R:Ramussen, U.B.; Wohlrad, H.
 Biochem. Biophys. Res. Commun. 138, 850-857, 1986
 A:Title: Bovine cardiac mitochondrial ADP/ATP-carrier: two distinct mRNAs and an unusual
 A:Reference number: A24822; MUID:86295775; PMID:3017341
 A:Accession: A24822
 A:Molecule type: mRNA
 A:Residues: 208-298 <RAS>
 A:Cross-references: GB:M13783; NID:g162630; PIDN:AAA30363.1; PID:g162631
 R:Aquila, H.; Mistr, D.; Eulitz, M.; Klingenberg, M.
 Hoppe-Seyler's Z. Physiol. Chem. 363, 345-349, 1982
 A:Title: Complete amino acid sequence of the ADP/ATP carrier from beef heart mitochondrion
 A:Reference number: A03181; MUID:82188267; PMID:7076130
 A:Accession: A03181
 A:Molecule type: protein
 A:Residues: 2-51, 'X', '53-70', 'X', '72-109', 'X', '111-298' <ADU>
 A:Note: residue 52 may be methyllysine
 R:Babel, W.; Wachter, E.; Aquila, H.; Klingenberg, M.
 Biochim. Biophys. Acta 670, 176-180, 1981
 A:Title: Amino acid sequence determination of the ADP/ATP carrier from beef heart mitochondrion
 A:Reference number: A61343; MUID:82046808; PMID:6271240
 A:Accession: A61343
 A:Molecule type: protein
 A:Residues: 205-298 <BAB>
 R:Oettmeier, W.; Masson, K.; Kalina, S.
 Eur. J. Biochem. 227, 730-733, 1995
 A:Title: [(3)H]-azido-4-isopropylacridone labels Cys159 of the bovine mitochondrial ADP
 A:Reference number: S69369; MUID:95172058; PMID:7867632
 A:Accession: S69369
 A:Molecule type: protein
 A:Residues: 49-63, 154-168 <OET>
 C:Comment: This protein is synthesized in the cytosol and transported into the mitochondrion
 C:Complex: homodimer
 C:Function:
 A:Note: catalyzes the exchange between cytosolic ADP and mitochondrial ATP genera
 C:Superfamily: ADP, ATP carrier protein; ADP, ATP carrier protein repeat homology
 C:Keywords: acetylated amino end; duplication; homodimer; methylated amino acid; mitoch
 F:5-99/Domain: ADP, ATP carrier protein repeat homology <ACP1>
 F:110-202/Domain: ADP, ATP carrier protein repeat homology <ACP2>
 F:207-298/Domain: ADP, ATP carrier protein repeat homology <ACP3>
 F:2/Modified site: acetylated amino end (Ser) (in mature form) #status experimental
 F:52/Modified site: N6-methyllysine (Lys) #status predicted

Query Match 91.7%; Score 1419; DB 1; Length 298;
 Best Local Similarity 89.6%; Pred. No. 1e-118;
 Matches 267; Conservative 16; Mismatches 14; Indels 0; Gaps 0;

Qy 1 MTDALSPAKDLFAGVAAATSKTAVARIEVKLLQVHASKQTADAKOKGIIIDCYVR 60
 Db 1 MSDQALSPKDLFAGVAAATSKTAVARIEVKLLQVHASKQTADAKOKGIIIDCYVR 60
 Qy 61 IPKEGVLSFWRGNLANVIRFPFOALNFAKDKYKQIFLGVDKHNQFMFRFAGNLASG 120
 Db 61 IPKEGVLSFWRGNLANVIRFPFOALNFAKDKYKQIFLGVDKHNQFMFRFAGNLASG 120
 Qy 121 GAAGATSLCFEYPLDFAFTRLADVGKAGAEERFGLDCLVKIKYSDGKGLYOGFNV 180
 Db 121 GAAGATSLCFEYPLDFAFTRLADVGKAGAEERFGLDCLVKIKYSDGKGLYOGFNV 180
 Qy 181 VGGIITIRAAVFGIYDTAKGMLPDPKNTNHYISWMIAGTVAVAGLSTPPDYARRMM 240
 Db 181 VGGIITIRAAVFGIYDTAKGMLPDPKNTNHYISWMIAGTVAVAGLSTPPDYARRMM 240
 Qy 241 OSGRKGTIDIMTYGTLDCWRKTLARDEGKAFKFGAMSNVLRMGCAFVLVLDKTK 297
 Db 241 OSGRKGTIDIMTYGTLDCWRKTLARDEGKAFKFGAMSNVLRMGCAFVLVLDKTK 297

RESULT 6

S37210

ADP, ATP carrier protein T1 - mouse

N:Alternate names: adenine nucleotide carrier

C:Species: Mus musculus (house mouse)

C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Aug-1999

C:Accession: S37210

R:Plaplace, C.; Costet, P.

submitted to the EMBL Data Library, September 1993

A:Reference number: S37210

A:Accession: S37210

A>Status: preliminary

A:Molecule type: mRNA

A:Residues: 1-298 <LAP>

A:Cross-references: EMBL:X74510; NID:g402627; PIDN:CAA52616.1; PID:g402628

A:Gene: ANCI

C:Superfamily: ADP, ATP carrier protein; ADP, ATP carrier protein repeat homology

C:Keywords: duplication; transmembrane protein

F:5-99/Domain: ADP, ATP carrier protein repeat homology <ACP1>

F:110-202/Domain: ADP, ATP carrier protein repeat homology <ACP2>

F:207-298/Domain: ADP, ATP carrier protein repeat homology <ACP3>

Query Match 91.6%; Score 1417; DB 2; Length 298;
 Best Local Similarity 89.6%; Pred. No. 1.5e-118;
 Matches 266; Conservative 15; Mismatches 16; Indels 0; Gaps 0;

Qy 1 MTDALSPAKDLFAGVAAATSKTAVARIEVKLLQVHASKQTADAKOKGIIIDCYVR 60
 Db 1 MTDALSPKDLFAGVAAATSKTAVARIEVKLLQVHASKQTADAKOKGIIIDCYVR 60
 Qy 61 IPKEGVLSFWRGNLANVIRFPFOALNFAKDKYKQIFLGVDKHNQFMFRFAGNLASG 120
 Db 61 IPKEGVLSFWRGNLANVIRFPFOALNFAKDKYKQIFLGVDKHNQFMFRFAGNLASG 120
 Qy 121 GAAGATSLCFEYPLDFAFTRLADVGKAGAEERFGLDCLVKIKYSDGKGLYOGFNV 180
 Db 121 GAAGATSLCFEYPLDFAFTRLADVGKAGAEERFGLDCLVKIKYSDGKGLYOGFNV 180
 Qy 181 VGGIITIRAAVFGIYDTAKGMLPDPKNTNHYISWMIAGTVAVAGLSTPPDYARRMM 240
 Db 181 VGGIITIRAAVFGIYDTAKGMLPDPKNTNHYISWMIAGTVAVAGLSTPPDYARRMM 240
 Qy 241 OSGRKGTIDIMTYGTLDCWRKTLARDEGKAFKFGAMSNVLRMGCAFVLVLDKTK 297
 Db 241 OSGRKGTIDIMTYGTLDCWRKTLARDEGKAFKFGAMSNVLRMGCAFVLVLDKTK 297

F:112-204/Domain: ADP, ATP carrier protein repeat homology <ACR2>
F:209-300/Domain: ADP, ATP carrier protein repeat homology <ACP3>

Query Match 75.6%; Score 1170; DB 1; Length 301;
Best Local Similarity 78.1%; Pred. No. 1,5e-96;
Matches 225; Conservative 18; Mismatches 45; Indels 0; Gaps 0;

QY 8 FAKDFLAGVAAAIKSTAVAPIERVKLLQVQHASQKQTADKQYGIIDCVIRIKREGEV 67
DB 10 FAKDFLAGVAAAIKSTAVAPIERVKLLQVQHASQKQTADKQYGIIDCVIRIKREGEV 69
QY 68 LSFMRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKRTQFWRFAGNLASGGAAGATS 127
DB 70 GAFCCGNLANVIRYPTQALNFAFKDKYKQIFLGVDKRTQFWRFAGNLASGGAAGATS 129
QY 128 LCFVYPLDFARTRLADYVKGAGAEERFGLDCLVKKIKYSDGINKLYOGFNVSVGGIITY 187
DB 130 LCFVYPLDFARTRLADYVKGAGAEERFGLDCLVKKIKYSDGINKLYOGFNVSVGGIITY 189
QY 188 RAAVFGIYDTAKGMLPDPKNTHTIVSMIAQTVTAAGLTSYFPDVTYRRMMQSGRKG 247
DB 190 RAAVFGIYDTAKGMLPDPKNTHTIVSMIAQTVTAAGLTSYFPDVTYRRMMQSGRKG 249
QY 248 DIMTGTGLDCWRKIARDGKAFKFGAMSNTLRGSGAFVLYLDEIKY 295
DB 250 EVMKNTLDCWKVTKIGKQSGAFKFGAMSNTLRGSGAFVLYLDEIKY 297

RESULT 10

T25371

hypothetical protein T27E9.1 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 11-Jan-2000

C:Accession: T25371

R: Lloyd, C.
submitted to the EMBL Data Library, November 1996

A:Reference number: Z20024

A:Accession: T25371

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-300 <M1>

A:Cross-references: EMBL:Z82059; PIDN:CA804874.1; GSPDB:GN00021; CESP:T27E9.1

A:Experimental source: clone T27E9

C:Genetics:

A:Gene: CESP:T27E9.1

A:Map position: 3

A:Introns: 20/1; 41/3; 115/2

C:Superfamily: ADP, ATP carrier protein; ADP, ATP carrier protein repeat homology

Query Match 66.7%; Score 1032; DB 2; Length 300;
Best Local Similarity 69.8%; Pred. No. 2.9e-84;
Matches 203; Conservative 34; Mismatches 50; Indels 4; Gaps 3;

QY 8 FAKDFLAGVAAAIKSTAVAPIERVKLLQVQHASQKQTADKQYGIIDCVIRIKREGEV 67
DB 12 FLIDIASGCTAAAVKSTAVAPIERVKLLQVQDASKAIAVDKRGIMVILRVPRKEGV 71
QY 68 LSFMRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKRTQFWRFAGNLASGGAAGATS 127
DB 72 AALMRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKRTQFWRFAGNLASGGAAGATS 131
QY 128 LCFVYPLDFARTRLADYVKGAGAEERFGLDCLVKKIKYSDGINKLYOGFNVSVGGIITY 187
DB 132 LCFVYPLDFARTRLADYVKGAGAEERFGLDCLVKKIKYSDGINKLYOGFNVSVGGIITY 190
QY 188 RAAVFGIYDTAKGMLPDPKNTHTIVSMIAQTVTAAGLTSYFPDVTYRRMMQSGRKG 246
DB 191 RAAVFGIYDTAKGMLPDPKNTHTIVSMIAQTVTAAGLTSYFPDVTYRRMMQSGRKG 249
QY 247 TDIMTGTGLDCWRKIARDGKAFKFGAMSNTLRGSGAFVLYLDEIKY 297
DB 250 DILYKNTLDCAKKIIONEGSAMFKGALSNTFRGTGALVLAITDEIOKF 299

RESULT 11

T23207

hypothetical protein K01H12.2 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 11-Jan-2000

C:Accession: T23207

R: McMurray, A.
submitted to the EMBL Data Library, December 1995

A:Reference number: Z19707

A:Accession: T23207

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-313 <M1>

A:Cross-references: EMBL:Z68218; PIDN:CAA92472.1; GSPDB:GN00022; CESP:K01H12.2

A:Experimental source: clone K01H12

C:Genetics:

A:Gene: CESP:K01H12.2

A:Map position: 4

A:Introns: 4/1; 191/2

C:Superfamily: ADP, ATP carrier protein; ADP, ATP carrier protein repeat homology

Query Match 66.5%; Score 1029; DB 2; Length 313;
Best Local Similarity 70.8%; Pred. No. 5.6e-84;
Matches 206; Conservative 28; Mismatches 53; Indels 4; Gaps 3;

QY 8 FAKDFLAGVAAAIKSTAVAPIERVKLLQVQHASQKQTADKQYGIIDCVIRIKREGEV 67
DB 25 FLIDIASGCTAAAVKSTAVAPIERVKLLQVQDASKAIAVDKRGIMVILRVPRKEGV 84
QY 68 LSFMRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKRTQFWRFAGNLASGGAAGATS 127
DB 85 AALMRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKRTQFWRFAGNLASGGAAGATS 144
QY 128 LCFVYPLDFARTRLADYVKGAGAEERFGLDCLVKKIKYSDGINKLYOGFNVSVGGIITY 187
DB 145 LCFVYPLDFARTRLADYVKGAGAEERFGLDCLVKKIKYSDGINKLYOGFNVSVGGIITY 203
QY 188 RAAVFGIYDTAKGMLPDPKNTHTIVSMIAQTVTAAGLTSYFPDVTYRRMMQSGRKG 246
DB 204 RAAVFGIYDTAKGMLPDPKNTHTIVSMIAQTVTAAGLTSYFPDVTYRRMMQSGRKG 262
QY 247 TDIMTGTGLDCWRKIARDGKAFKFGAMSNTLRGSGAFVLYLDEIKY 297
DB 263 DILYKNTLDCAKKIIONEGSAMFKGALSNTFRGTGALVLAITDEIOKF 312

RESULT 12

T25850

hypothetical protein T01B11.4 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans

C:Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 11-Jan-2000

C:Accession: T25850

R: Geisel, C.; Stellyes, L.
submitted to the EMBL Data Library, December 1996

A:Description: The sequence of C. elegans cosmid T01B11.

A:Reference number: Z20099

A:Accession: T25850

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-313 <GE1>

A:Cross-references: EMBL:U80931; PIDN:AAB38001.1; GSPDB:GN00022; CESP:T01B11.4

A:Experimental source: strain Bristol N2; clone T01B11

C:Genetics:

A:Gene: CESP:T01B11.4

A:Map position: 4

A:Introns: 4/1; 191/2

C:Superfamily: ADP, ATP carrier protein; ADP, ATP carrier protein repeat homology

Query Match 66.5%; Score 1029; DB 2; Length 313;
Best Local Similarity 70.8%; Pred. No. 5.6e-84;
Matches 206; Conservative 28; Mismatches 53; Indels 4; Gaps 3;


```

Db      63 RVSKEQVLSLMRGVANVIRFPYQAFNFAKDYFKNIF-PRYDONTDFSKFPCVNILS 121
QY      120 GGAAGATSLCFVYPLDFAFTRILADYVGKAGAREFERGLDCLVKIYKSDGIRGLYOGFNV 179
      122 GATAGATISLLIYPLDFAFTRILASDICK-GKDRQFTGLFDCLAKTIYKQTGILSLISGFCV 180
Db      180 SVQGIITIRAAVEFGIYDTAKGML-PDPKNTIIVISMMIAQVTAVAGLTSYPPDVTVRRRM 238
      181 SVTGIIYVYRGSYFGLYDSAKALLFTNDKNTIIVLKWAVASVYIILAGLISYPPDVTVRRRM 240
QY      239 MMQSGRKG-TDIMYTGTLDCMRKTIARDEGKAFKFGAMSNNLRGAGAFVLYLYDEIKK 296
Db      241 MMMSGRKKEEIQYKNTIDCWIKILRNESFGKFGKAWANVIRGAGGALVLYFYDELOK 299

```

Search completed: August 28, 2003, 19:43:17
 Job time : 20.6898 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 28, 2003, 19:28:06 ; Search time 12.0134 Seconds

(without alignments)
1166.524 Million cell updates/sec

Title: US-09-811-132-32

Perfect score: 1547

Sequence: 1 MTDALSLFAKDFLAGVAAA.....LRGMGAFVLVYDEIKRYT 298

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | ID | Description |
|------------|--------|-------------|--------|-------------|--------------------|
| 1 | 1537 | 99.4 | 298 | ADP2_HUMAN | P05141 homo sapien |
| 2 | 1525 | 98.6 | 298 | ADP2_RAT | Q09073 rattus norv |
| 3 | 1519 | 98.2 | 298 | ADP2_MOUSE | P51881 mus musculu |
| 4 | 1458 | 94.2 | 298 | ADP3_BOVIN | P32007 bos taurus |
| 5 | 1454 | 94.0 | 298 | ADP3_HUMAN | P12236 homo sapien |
| 6 | 1417 | 91.6 | 298 | ADP1_MOUSE | P48962 mus musculu |
| 7 | 1417 | 91.6 | 298 | ADP1_RAT | Q05622 rattus norv |
| 8 | 1414 | 91.4 | 297 | ADP1_BOVIN | P02722 bos taurus |
| 9 | 1413 | 91.3 | 298 | ADP1_HUMAN | P12235 homo sapien |
| 10 | 1253.5 | 81.0 | 299 | ADP_DROME | Q26365 drosophila |
| 11 | 1190 | 76.9 | 301 | ADP_ANOGA | Q27368 anopheles g |
| 12 | 968 | 62.6 | 339 | ADP_CHLKE | P31692 chlorella k |
| 13 | 771 | 49.8 | 386 | ADP1_GOSHI | Q22342 gossypium h |
| 14 | 770 | 49.8 | 322 | ADP_SCHPO | Q09188 schizosacch |
| 15 | 765 | 49.5 | 308 | ADP_CHLRE | P27080 chlamydomon |
| 16 | 761.5 | 49.2 | 387 | ADP3_YEAST | P18238 saccharomyc |
| 17 | 759 | 48.9 | 313 | ADP1_MAIZE | P04709 zea mays (m |
| 18 | 757 | 48.9 | 385 | ADP2_ARATH | P40941 arabidopsis |
| 19 | 753.5 | 48.7 | 387 | ADP2_ARATH | P12857 zea mays (m |
| 20 | 753 | 48.7 | 387 | ADP2_YEAST | P25083 solanum tub |
| 21 | 752.5 | 48.6 | 318 | ADP2_YEAST | P31691 oryza sativ |
| 22 | 752 | 48.6 | 386 | ADP1_SOLITU | P43191 kluyveromyc |
| 23 | 750 | 48.5 | 382 | ADP_ORYSA | P31167 arabidopsis |
| 24 | 749.5 | 48.4 | 305 | ADP1_KLUTA | Q4129 triticum ae |
| 25 | 747.5 | 48.3 | 381 | ADP1_ARATH | P27081 solanum tub |
| 26 | 744 | 48.1 | 331 | ADP1_WHEAT | Q4130 triticum ae |
| 27 | 741.5 | 47.9 | 386 | ADP2_SOLITU | P04710 saccharomyc |
| 28 | 737 | 47.6 | 331 | ADP2_WHEAT | P19529 caenorhabdi |
| 29 | 728 | 47.1 | 309 | ADP1_YEAST | Q20799 caenorhabdi |
| 30 | 312.5 | 20.2 | 565 | CMG3_CAEEL | Q01888 bos taurus |
| 31 | 307 | 19.8 | 588 | CMG2_CAEEL | Q09297 saccharomyc |
| 32 | 285 | 18.4 | 330 | GDC_BOVIN | |
| 33 | 284 | 18.4 | 307 | ODC2_YEAST | |

| | | | | | | |
|----|-------|------|-----|---|------------|--------------------|
| 34 | 278 | 18.0 | 325 | 1 | UCP5_MOUSE | Q922b2 mus musculu |
| 35 | 276.5 | 17.9 | 322 | 1 | GDC_RAT | P16261 rattus norv |
| 36 | 276.5 | 17.9 | 702 | 1 | CMC1_CAEEL | Q21153 caenorhabdi |
| 37 | 276 | 17.8 | 678 | 1 | CMC1_HUMAN | Q95746 homo sapien |
| 38 | 274 | 17.7 | 325 | 1 | UCP5_HUMAN | Q95258 homo sapien |
| 39 | 265.5 | 17.2 | 332 | 1 | GDC_HUMAN | P16260 homo sapien |
| 40 | 265 | 17.1 | 306 | 1 | CMN9_MOUSE | Q8b103 mus musculu |
| 41 | 261.5 | 16.9 | 675 | 1 | CMN2_HUMAN | Q9450 homo sapien |
| 42 | 261 | 16.9 | 310 | 1 | ODC1_YEAST | Q03028 saccharomyc |
| 43 | 257.5 | 16.6 | 315 | 1 | MPL_HUMAN | Q9b2d1 homo sapien |
| 44 | 256 | 16.5 | 303 | 1 | CMN6_HUMAN | Q8b8r3 homo sapien |
| 45 | 249.5 | 16.1 | 326 | 1 | YB08_SCHPO | O13805 schizosacch |

ALIGNMENTS

RESULT 1
ADP2_HUMAN STANDARD; PRT; 298 AA.
ID AC P05141; O43350;
DT 13-AUG-1987 (rel. 05, Created)
DT 01-OCT-1994 (rel. 30, Last sequence update)
DT 28-FEB-2003 (rel. 41, Last annotation update)
DE ADP, ATP carrier protein, fibroblast isoform (ADP/ATP translocase 2)
DE (Adenine nucleotide translocator 2) (ANT 2).
GN SLC25A5 OR ANT2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Placenta;
RX MEDLINE=90375457; PubMed=2168878;
RA Ku D.-H., Kagan J., Chen S.-T., Chang C.-D., Baserga R., Wurzel J.;
RT "The human fibroblast adenine nucleotide translocator gene. Molecular
RT cloning and sequence."
RL J. Biol. Chem. 265:16060-16063(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=87166056; PubMed=3031073;
RA Battini R., Ferrarri S., Kaczmarek L., Calabretta B., Chen S.T.,
RA Baserga R.;
RT "Molecular cloning of a cDNA for a human ADP/ATP carrier which is
RT growth-regulated."
RL J. Biol. Chem. 262:4355-4358(1987).
RN [3]
RP SEQUENCE FROM N.A.
RX Chen C.N., Su Y., Baybayan P., Siruno A., Nagara J. R.,
RA Mazarella R.A., Schlessinger D., Chen E.Y.;
RT Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RX Becker M., Graves T., Ozersky P.;
RT Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE OF 47-298 FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=88124845; PubMed=2829183;
RA Houldsworth J., Attardi G.;
RT "Two distinct genes for ADP/ATP translocase are expressed at the mRNA
RT level in adult human liver."
RL Proc. Natl. Acad. Sci. U.S.A. 85:377-381(1988).
CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
CC MITOCHONDRIAL INNER MEMBRANE.
CC -1- SUBUNIT: Homodimer.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC inner membrane.
CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
CC
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| | | | | | |
|----|----------|----------------------|--------------------------------|------------------------|---------------------------|
| | DR | EMBL; J07424; | AAA51737.1. | - | |
| | DR | EMBL; M5683; | AAAS5579.1. | - | |
| | DR | EMBL; L78810; | AAB39266.1. | - | |
| | DR | EMBL; AC004000; | AAB96347.1. | - | |
| | DR | PIR; A29132; | AAA36749.1. | - | |
| | DR | Genev; HGNC: | I099132. | SLOC25A5. | |
| | DR | MIM; 300150; | - | | |
| | DR | GO; GO:0005887; | C:integral to plasma membrane; | TAS. | |
| | DR | GO; GO:0015207; | Fadeline transporter activity; | TAS. | |
| | DR | GO; GO:0006832; | Pisamm molecule transport; | TAS. | |
| | DR | InterPro; IPR002067; | Mt_carrier. | | |
| | DR | InterPro; IPR002030; | Mit_uncoupling. | | |
| | DR | Interpro; IPR001993; | MitoCh_carrter. | | |
| | DR | Pfam; PF00193; | mico_carr_3. | | |
| | DR | PRINTS; PRD0926; | MITOCARRIER. | | |
| | DR | PRINTS; PRO0784; | MTUNCOUPLING. | | |
| | DR | PROSITE; PS00215; | MITOCH_CARRIER. | 3. | |
| KW | DM | mitochondrion; | Inner membrane; | Repeat; | Transmembrane; Transport; |
| KM | RV | Multigene family. | | | |
| FT | ET | TRANSMEM | 12 | 29 | 1 (POTENTIAL). |
| FT | ET | TRANSMEM | 73 | 91 | 2 (POTENTIAL). |
| FT | ET | TRANSMEM | 117 | 134 | 3 (POTENTIAL). |
| FT | ET | TRANSMEM | 176 | 195 | 4 (POTENTIAL). |
| FT | ET | TRANSMEM | 214 | 231 | 5 (POTENTIAL). |
| FT | ET | TRANSMEM | 273 | 291 | 6 (POTENTIAL). |
| FT | REPEAT | REPEAT | 1 | 111 | 1. |
| FT | REPEAT | REPEAT | 112 | 208 | 2. |
| FT | REPEAT | REPEAT | 209 | 298 | 3. |
| FT | CONFLICT | CONFLICT | 66 | 66 | V -> L (IN REF. 2). |
| FT | CONFLICT | CONFLICT | 111 | 111 | G -> E (IN REF. 2). |
| FT | CONFLICT | CONFLICT | 162 | 162 | R -> L (IN REF. 4 AND 5). |
| DQ | SEQUENCE | 298 AA; | 32895 MM; | FYJ3CAEDN2C49D3 CRC64; | V -> G (IN REF. 5). |

| | | | | |
|---------------------------|-------|---------------------|-----------|-------------|
| Query Match | 99.4% | Score 1537 | DB 1: | Length 298; |
| Best Local Similarity | 99.3% | Pred. NC: 8.9e-128; | | |
| Matches 296; Conservative | 1; | Mismatches 1; | Indels 0; | Gaps 0; |

[illegible]

| RESULT 2 | | |
|----------|-------------|---------------------------------|
| ADT2_RAT | ID | STANDARD; PRT; 298 AA |
| AC | 009073; | |
| DT | 01-FEB-1995 | (Rel. 31, Created) |
| DT | 01-FEB-1995 | (Rel. 31, Last sequence update) |

DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE ADP/ATP carrier protein, fibroblast isoform (ADP/ATP translocase 2)
 DE (Adenine nucleotide translocator 2) (ANT 2).
 GN SLIC25A5 OR ANT2.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus
 ON NCBI_TaxID=10116;

KN
 LN
 RP SEQUENCE FROM N.A.
 RC STRAIN-Sprague-Dawley; TISSUE-Liver;
 RX MEDLINE-94002161; PubMed-8399300;
 RA Shinohara Y., Kamida M., Yamazaki N., Terada H.;
 RL Biochim. Biophys. Acta 1152:192-196(1993).
 RT "Isolation and characterization of cDNA clones and a genomic clone
 RT encoding rat mitochondrial adenine nucleotide translocator.";
 CC 1-10-1 FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
 CC MITOCHONDRIAL INNER MEMBRANE.
 CC 1-1 SUBUNIT: Homodimer.
 CC 1-1 SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
 CC inner membrane.
 CC 1-1 TISSUE SPECIFICITY: PRESENT IN KIDNEY, BRAIN, HEART, LIVER AND
 CC SKELETAL MUSCLE.
 CC 1-1 DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
 CC 1-1 SIMILARITY: Belongs to the mitochondrial carrier family.
 CC -----
 CC CC THIS SWISS-PROT entry is copyright. It is produced through a collaboration
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| CC | EMBL | D12771 | BAA02238.1 | - |
|----|--|-----------|--------------------|-------------------------|
| DR | InterPro | IPR002067 | Mit_carrier. | |
| DR | InterPro | IPR002030 | Mit_uncoupling. | |
| DR | InterPro | IPR001993 | Mitoch_carrier. | |
| DR | Pfam | PF00153 | mito_carrt; 3. | |
| DR | PRINTS | PR00926 | MITOCARRIER. | |
| DR | PRINTS | PR00784 | MTUNCOUPLING. | |
| DR | PROSITE | PS00215 | MITOCH_CARRIER; 3. | |
| KW | Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport; | | | |
| MM | Multigene family. | | | |
| FT | TRANSMEM | 12 | 29 | 1 (POTENTIAL). |
| FT | TRANSMEM | 73 | 91 | 2 (POTENTIAL). |
| FT | TRANSMEM | 117 | 134 | 3 (POTENTIAL). |
| FT | TRANSMEM | 176 | 195 | 4 (POTENTIAL). |
| FT | TRANSMEM | 214 | 231 | 5 (POTENTIAL). |
| FT | TRANSMEM | 273 | 291 | 6 (POTENTIAL). |
| FT | REPEAT | 1 | 111 | 1 |
| FT | REPEAT | 112 | 208 | 2. |
| FT | REPEAT | 209 | 298 | 3. |
| QC | SEQUENCE | 298 AA; | 32901 MW; | 6A59204B987EEB35 CRC64; |

| | | | | |
|-----------------------|----------------|------------------|----------|------------|
| Query Match | 98.6% | Score 1525 | DB 1 | Length 298 |
| Best Local Similarity | 98.3% | Pred. No. 1e-126 | | |
| Matches 293 | Conservative 3 | Mismatches 2 | Indels 0 | Gaps 0 |

QY 1 MTDAAISFAKDFLAGVAAAISKTAVAPIERVKLLLOVHASKOITADOKOYGIIIDCVR 60
| | | | : | | | | : | | | | : | | | | : | | | | : | | | | : | | | | : | | | | :
Db 1 MTDAAVSFADFFLAGVAAAISKTAVAPIERVKLLLOVHASKOITADOKOYGIIIDCVR 60

QY 61 IPKEOEVLSPWGRGNLANAVIRYPPTQALNFAFKDKYKOLFGLGVDRKTQFMRYEAGNLASG 120
| | | | : | | | | : | | | | : | | | | : | | | | : | | | | : | | | | : | | | | :
Db 61 IPKEOGVLSFWRGRLANAVIRYFPPTQALNFAFKDKYKOLFGLGVDRKTQFMRYEAGNLASG 120

QY 121 GAAGATSLCFYPLDPAFTRIADLVAKGAEREFRGLGDCLVIKYKSDGIKGLYQGPNVS 180
| | | | : | | | | : | | | | : | | | | : | | | | : | | | | : | | | | : | | | | :
Db 121 GAAGATSLCFYPLDPAFTRIADLVAKGAEREFRGLGDCLVIKYKSDGIKGLYQGPNVS 180

QY 181 VGGIITIRAAVFGLYDPAKGMLPDPKNTHTYISMIAQTYSANAAGLSTYEPDIYRRRMM 240
| | | | : | | | | : | | | | : | | | | : | | | | : | | | | : | | | | : | | | | :

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DB      181 VGGIIYRAAYFGIYDPAKGMIPDKNTHIFISWIAOSVTAAGITSTPDTVRRMM 240
QY      241 OSGRKGTDMYGTGLDCKRKIARDGSKAFKFGAMSNVLRGGAFLVLYDEIRKKT 298
DB      241 OSGRKGTDMYGTGLDCKRKIARDGSKAFKFGAMSNVLRGGAFLVLYDEIRKKT 298

RESULT 3
ADT2_MOUSE STANDARD: PRT: 298 AA.
AC      P51881.061311.
DT      01-OCT-1996 (Rel. 34, Created)
DT      01-OCT-1996 (Rel. 34, Last sequence update)
DE      28-FEB-2003 (Rel. 41, Last annotation update)
DE      ADP,ATP carrier protein, fibroblast isoform (ADP/ATP translocase 2)
DE      (Adenine nucleotide translocator 2) (ANT 2).
GN      SLG25A5 OR ANT2.
OS      Mus musculus (Mouse).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
OX      NCBI_TaxID=10090;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      STRAIN=C57BL/6; TISSUE=Brain;
RX      MEDLINE=97059403; PubMed=8903724;
RA      Ellison J.W., Li X., Francke U., Shapiro L.J.;
RT      "Rapid evolution of human pseudautosomal genes and their mouse
RT      homologs."
RL      Mamm. genome 7:25-30(1996).
RN      [2]
RP      SEQUENCE FROM N.A.
RC      TISSUE=Skeletal muscle;
RA      Sheldon J.G.;
RL      Theis (1995), University of Cambridge, U.K.
RN      [3]
RP      SEQUENCE FROM N.A.
RC      STRAIN=129/SV;
RA      Costet P., Laplace C.;
RL      Submitted (FEB-1993) to the EMBL/Genbank/DBJ databases.
RN      [4]
RP      REVISIONS.
RA      Laplace C.;
RL      Submitted (FEB-1997) to the EMBL/Genbank/DBJ databases.
RN      [5]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=20432087; PubMed=10974536;
RA      Levy S.E., Chen Y.-S., Graham B.H., Wallace D.C.;
RT      "Expression and sequence analysis of the mouse adenine nucleotide
RT      translocase 1 and 2 genes."
RL      Gene 254:57-66(2000).
CC      -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
CC      MITOCHONDRIAL INNER MEMBRANE.
CC      -1- SUBUNIT: Homodimer.
CC      -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC      inner membrane.
CC      -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC      -1- SIMILARITY: Belongs to the mitochondrial carrier family.
CC      -----
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CC      entities requires a license agreement (see http://www.isb-sib.ch/announce/
CC      or send an email to license@sib-sib.ch).
CC      -----
DR      EMBL: U27316; AAC52838.1; -
DR      EMBL: U10404; AAA19009.1; -
DR      EMBL: X70847; CAA50196.1; -
DR      EMBL: AF240003; AAF64471.1; -
DR      MGD: MGI:1353496; SLC25A5.
DR      InterPro: IPR002067; Mtc_carrier.
DR      InterPro: IPR002030; Mtc_uncoupling.

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DR      InterPro: IPR001993; MitoCh_carrier.
DR      Pfam: PF00153; Mito_carr_3.
DR      PRINTS: PR00926; MITOCARRIER.
DR      PRINTS: PR00784; MTUNCOUPLING.
DR      PROSITE: PS00215; MITOCH_CARRIER; 3.
KW      Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
KW      Multigene family.
FT      TRANSMEM 12 29 1 (POTENTIAL).
FT      TRANSMEM 73 91 2 (POTENTIAL).
FT      TRANSMEM 117 134 3 (POTENTIAL).
FT      TRANSMEM 176 195 4 (POTENTIAL).
FT      TRANSMEM 214 231 5 (POTENTIAL).
FT      TRANSMEM 273 291 6 (POTENTIAL).
FT      REPEAT 1 111 1.
FT      REPEAT 112 208 2.
FT      REPEAT 209 298 3.
SQ      SEQUENCE 298 AA: 32931 MW: 0798E04B987EE20 CRC64;

Query Match      98.2%; Score 1519; DB 1; Length 298;
Best Local Similarity 98.0%; Pred. No. 3.4e-126;
Matches 292; Conservative 3; Mismatches 3; Indels 0; Gaps 0;

QY      1 MTDAAISFKDPLAGGVAIAISKTAVAPIERYKLLQVOHASKQITADKQYGIIDCVVR 60
DB      1 MTDAAVSFAKDFLAGGVAIAISKTAVAPIERYKLLQVOHASKQITADKQYGIIDCVVR 60
QY      61 IPKEGVSEFMRGNLANVRYRPTQALNFAFDKTKQIFLGVDKRTQFWRFAFNLSG 120
DB      61 IPKEGVSEFMRGNLANVRYRPTQALNFAFDKTKQIFLGVDKRTQFWRFAFNLSG 120
QY      121 GAAGATSLCFVYPLDFARTRLADYGVKAGAEERFGLDCLVKIKYSDSINKLYOGFNV 180
DB      121 GAAGATSLCFVYPLDFARTRLADYGVKAGAEERFGLDCLVKIKYSDSINKLYOGFNV 180
QY      181 VGGIIYRAAYFGIYDPAKGMIPDKNTHIFISWIAOCTVAVAGITSTPDTVRRMM 240
DB      181 VGGIIYRAAYFGIYDPAKGMIPDKNTHIFISWIAOCTVAVAGITSTPDTVRRMM 240
QY      241 OSGRKGTDMYGTGLDCKRKIARDGSKAFKFGAMSNVLRGGAFLVLYDEIRKKT 298
DB      241 OSGRKGTDMYGTGLDCKRKIARDGSKAFKFGAMSNVLRGGAFLVLYDEIRKKT 298

RESULT 4
ADT3_BOVIN STANDARD: PRT: 298 AA.
AC      P32007.
DT      01-JUL-1993 (Rel. 26, Created)
DT      01-JUL-1993 (Rel. 26, Last sequence update)
DT      16-OCT-2001 (Rel. 40, Last annotation update)
DE      ADP,ATP carrier protein, isoform T2 (ADP/ATP translocase 3) (Adenine
DE      nucleotide translocator 3) (ANT 3).
GN      SLG25A6 OR ANT3.
OS      Bos taurus (Bovine).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC      Bovidae; Bovinae; Bos.
OX      NCBI_TaxID=9913;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=89229093; PubMed=2540808;
RA      Powell S.J., Medd S.M., Runswick M.J., Walker J.E.;
RT      "Two bovine genes for mitochondrial ADP/ATP translocase expressed
RT      differences in various tissues."
RL      Biochemistry 28:866-873(1989).
CC      -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
CC      MITOCHONDRIAL INNER MEMBRANE.
CC      -1- SUBUNIT: Homodimer.
CC      -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC      inner membrane.
CC      -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC      -1- SIMILARITY: Belongs to the mitochondrial carrier family.
CC      -----

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DR Pfam; PF00153; mito_carr; 3.
 DR PRINTS; PR00926; MITOCARRIER.
 DR PRINTS; PR00784; MTUNCOUPLING.
 DR PROSITE; PS00215; MITOCH_CARRIER; 3.
 KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
 KM Multigene family.
 FT TRANSMEM 12 29 1 (POTENTIAL).
 FT TRANSMEM 73 91 2 (POTENTIAL).
 FT TRANSMEM 117 134 3 (POTENTIAL).
 FT TRANSMEM 176 195 4 (POTENTIAL).
 FT TRANSMEM 214 231 5 (POTENTIAL).
 FT TRANSMEM 273 291 6 (POTENTIAL).
 FT REPEAT 1 100 1.
 FT REPEAT 101 208 2.
 FT REPEAT 209 298 3.
 FT REPEAT 105 108 3.
 FT CONFLICT 242 242 S -> F (IN REF. 3; AAH14775).
 FT CONFLICT 242 242 S -> F (IN REF. 3; AAH14775).
 SQ SEQUENCE 298 AA: 32866 MW: 1853459 F0E49672F CRC64;
 Query Match 94.0%; Score 1454; DB 1; Length 298;
 Best Local Similarity 92.6%; Pred. No. 1.7e-120;
 Matches 274; Conservative 13; Mismatches 9; Indels 0; Gaps 0;
 QY 1 MTDAAISPAKDFLAGVAAISKRAVADIERVKLLQVHASKQITADKQKGIIDCYVR 60
 DB 1 MTEQAISPAKDFLAGVAAISKRAVADIERVKLLQVHASKQITADKQKGIIDCYVR 60
 QY 61 IPKROEVSEFWRGNLANVIRYEPFOALNFAFRDKYKQIFLGVDKRRTOFMRYEAGNLSG 120
 DB 61 IPKROEVSEFWRGNLANVIRYEPFOALNFAFRDKYKQIFLGVDKRRTOFMRYEAGNLSG 120
 QY 121 GAAGATSLCEFYPLDFARTRLADVGKAGAEERFGLDCLVKIKYSGDKIGLYOGFNVS 180
 DB 121 GAAGATSLCEFYPLDFARTRLADVGKAGAEERFGLDCLVKIKYSGDKIGLYOGFNVS 180
 QY 121 GAAGATSLCEFYPLDFARTRLADVGKAGAEERFGLDCLVKIKYSGDKIGLYOGFNVS 180
 DB 121 GAAGATSLCEFYPLDFARTRLADVGKAGAEERFGLDCLVKIKYSGDKIGLYOGFNVS 180
 QY 181 VGGITTTAAATFGIYDTAKGMLPDKNTHIYISMKIACTVAVAGLTSYPEDTVRRMM 240
 DB 181 VGGITTTAAATFGIYDTAKGMLPDKNTHIYISMKIACTVAVAGLTSYPEDTVRRMM 240
 QY 241 QSGRKGDTIMTGTLDCKRKIARDEGGRKAFKAGANSVLRGGAFFVLYLDEIRK 296
 DB 241 QSGRKGDTIMTGTLDCKRKIARDEGGRKAFKAGANSVLRGGAFFVLYLDEIRK 296
 DB 241 QSGRKGDTIMTGTLDCKRKIARDEGGRKAFKAGANSVLRGGAFFVLYLDEIRK 296
 RESULT 6
 ADT1_MOUSE STANDARD: PRT: 298 AA.
 AC P48962; 062164;
 DT 01-FEB-1996 (Rel. 33, Created)
 DT 15-SEP-2003 (Rel. 42, Last sequence update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE ADP/ATP carrier protein, heart/skeletal muscle isoform T1 (ADP/ATP translocase 1) (Adenine nucleotide translocator 1) (ANT 1) (mANT1).
 GN SLC25A4 OR ANT1 OR ANCL1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sclurognathi; Muridae; Murinae; Mus.
 OC NCBI_TaxID=10090;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=C57BL/6; TISSUE=Brain;
 RX MEDLINE=97059403; PubMed=8903724;
 RA Ellison J.W., Li X., Francke U., Shapiro L.J.;
 RT "Rapid evolution of human pseudautosomal genes and their mouse homologs";
 RL Mamm. Genome 7:25-30(1996).
 RN [2]
 RP SEQUENCE FROM N.A.
 RC STRAIN=BALB/c; TISSUE=Muscle;
 RA Laplace C., Costet P.;
 RL Submitted (SEP-1993) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.

RA Levy S.E., Chen Y.-S., Graham B.H., Wallace D.C.;
 RT "Expression and sequence analysis of the mouse adenine nucleotide translocase 1 and 2 genes";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Eye;
 RX MEDLINE=22388257; PubMed=12477932;
 RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D., Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K., Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F., Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L., Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Prange C., Brownstein M.J., Usdin T.B., Toshiyuki S., Carolini P., Scheetz T.E., Rabe S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J., Bosak S.A., McEwan P.J., McKernan K.O., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahy J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Buterfield Y.S.N., Krzywinski M.I., Skalska U., Smallus D.E., Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
 RT "Generation and initial analysis of more than 15,000 full-length human and mouse cDNA sequences";
 RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
 CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE MITOCHONDRIAL INNER MEMBRANE.
 CC -1- SUBUNIT: Homodimer.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial inner membrane.
 CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
 CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
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 CC
 DR EMBL; U27315; AAC52837.1; -;
 DR EMBL; X74510; CA52616.1; -;
 DR EMBL; AF240002; AAF64470.1; -;
 DR EMBL; BC003791; AAH03791.1; -;
 DR EMBL; BC026925; AAH26925.1; -;
 DR PIR; S37210; S37210.
 DR MGD; MGI:1353495; SLC25A4.
 DR InterPro; IPR002067; Mtc_carrier.
 DR InterPro; IPR002030; Mtc_uncoupling.
 DR InterPro; IPR001993; Mitochl_carrier.
 DR Pfam; PF00153; mito_carr; 3.
 DR PRINTS; PR00926; MITOCARRIER.
 DR PRINTS; PR00784; MTUNCOUPLING.
 DR PROSITE; PS00215; MITOCH_CARRIER; 3.
 KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
 KM Multigene family.
 FT TRANSMEM 12 29 1 (POTENTIAL).
 FT TRANSMEM 73 91 2 (POTENTIAL).
 FT TRANSMEM 117 134 3 (POTENTIAL).
 FT TRANSMEM 176 195 4 (POTENTIAL).
 FT TRANSMEM 214 231 5 (POTENTIAL).
 FT TRANSMEM 273 291 6 (POTENTIAL).
 FT REPEAT 1 110 1.
 FT REPEAT 101 208 2.
 FT REPEAT 209 298 3.
 FT CONFLICT 136 136 F -> L (IN REF. 1).
 FT CONFLICT 136 136 F -> L (IN REF. 1).
 SQ SEQUENCE 298 AA: 32904 MW: 3A849FAB0981462 CRC64;
 Query Match 91.6%; Score 1417; DB 1; Length 298;


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RT an unusually short 3'-noncoding sequence."
RL Biochem. Biophys. Res. Commun. 138:850-857(1986).
CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
CC MITOCHONDRIAL INNER MEMBRANE.
CC -1- SUBUNIT: Homodimer.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC inner membrane.
CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
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CC -----
DR EMBL: M13783; AAA30363.1; -
DR EMBL: M24102; AAA30768.1; -
DR PIR: A43646; XMO.
DR InterPro: IPR002067; Mlt_carrier.
DR InterPro: IPR002030; Mlt_uncoupling.
DR InterPro: IPR001993; Mitoch_carrier.
DR Pfam: PF00153; mltc_carr; 3.
DR PRINTS: PR00926; MITOCARRIER.
DR PROSITE: PS00215; MITOCH_CARRIER; 3.
DR Mitochondrion: Inner membrane. Repeat; Transmembrane; Transport;
KW Multigene family; Methylation.
FT INIT_MET 0 0
FT MOD_RES 1 1 BLOCKED.
FT MOD_RES 51 51 METHYLATION (POTENTIAL).
FT TRANSMEM 11 28 1 (POTENTIAL).
FT TRANSMEM 72 90 2 (POTENTIAL).
FT TRANSMEM 116 133 3 (POTENTIAL).
FT TRANSMEM 175 194 4 (POTENTIAL).
FT TRANSMEM 213 230 5 (POTENTIAL).
FT TRANSMEM 272 290 6 (POTENTIAL).
FT REPEAT 1 110 1.
FT REPEAT 111 207 2.
FT REPEAT 208 297 3.
SQ SEQUENCE 297 AA: 32836 MW: A582D3C4A40AEB48 CRC64;
Query Match 91.4%; Score 1414; DB 1; Length 297;
Best Local Similarity 89.9%; Pred. No. 5,6e-117;
Matches 266; Conservative 16; Mismatches 14; Indels 0; Gaps 0;

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DT 01-OCT-1989 (rel. 12, Created)
DT 01-NOV-1990 (rel. 16, Last sequence update)
DT 15-SEP-2003 (rel. 42, Last annotation update)
DE ADP/ATP carrier protein, heart/skeletal muscle isoform T1 (ADP/ATP
DE translocase 1) (adenine nucleotide translocator 1) (ANT 1).
GN SL25A4 OR ANT1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE=89236396; PubMed=2541251;
RA Cozens A.L., Runswick M.J., Walker J.E.;
RT "DNA sequences of two expressed nuclear genes for human mitochondrial
RT ADP/ATP translocase."
RL J. Mol. Biol. 206:261-280(1989).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=89340499; PubMed=2547778;
RA Li R., Warner C.K., Hodge J.A., Minoshima S., Kudoh J.,
RA Fukuyama R., Maekawa M., Shimizu Y., Shimizu N., Wallace D.C.;
RT "A human muscle adenine nucleotide translocator gene has four exons,
RT is located on chromosome 4, and is differentially expressed."
RL J. Biol. Chem. 264:13998-14004(1989).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE=88041149; PubMed=2823266;
RA Neckelmann N., Li K., Wade R.P., Shuster R., Wallace D.C.;
RT "cDNA sequence of a human skeletal muscle ADP/ATP translocator: lack
RT of a leader peptide, divergence from a fibroblast translocator cDNA,
RT and coevolution with mitochondrial DNA genes."
RL Proc. Natl. Acad. Sci. U.S.A. 84:7580-7584(1987).
RN [4]
RP SEQUENCE FROM N.A.
RX MEDLINE=22388257; PubMed=12477932;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosak S.A., McMan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.W., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahney J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butlerfield Y.S.N., Krzywinski M.T., Skalska U., Smalins D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [5]
RP SEQUENCE OF 1-37 FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=88124845; PubMed=2829183;
RA Houldsworth J., Attardi G.;
RT "Two distinct genes for ADP/ATP translocase are expressed at the mRNA
RT level in adult human liver."
RL Proc. Natl. Acad. Sci. U.S.A. 85:377-381(1988).
RN [6]
RP VARIANTS PRO-114 AND MET-289.
RX MEDLINE=20385067; PubMed=10926541;
RA Kaukonen J., Jusselius J.K., Tiranit V., Kyttälä A., Zeviani M.,
RA Comi G.P., Keranen J., Peltonen L., Suomalainen A.;
RT "Role of adenine nucleotide translocator 1 in mtDNA maintenance."
RL Science 289:782-785(2000).
CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE

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CC MITOCHONDRIAL INNER MEMBRANE.
CC -1- SUBUNIT: Homodimer.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC inner membrane.
CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -1- DISEASE: Defects in SLC25A4 are a cause of autosomal dominant
CC progressive external ophthalmoplegia with various mitochondrial
CC DNA deletions (PEO). Patients with PEO have mitochondrial
CC myopathy, progressive external ophthalmoplegia, and other
CC abnormalities associated with multiple different deletions of
CC mitochondrial DNA.
CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
CC -----
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CC -----
CC EMBL: J02966; AAA61223.1; -
CC EMBL: J03593; AAA36751.1; -
CC EMBL: J04982; AAA51736.1; -
CC EMBL: BC008664; AA008664.1; -
CC PIR: A44778; A44778.
CC Genew: HGNC:10990; SLC25A4.
CC MIM: 157640; -
CC GO: GO:0005887; C:Mitochondrion; TAS.
CC GO: GO:0005739; C:Mitochondrion; TAS.
CC GO: GO:0015207; F:adenine transporter activity; TAS.
CC GO: GO:0006091; P:energy pathways; TAS.
CC GO: GO:0000002; P:mitochondrial genome maintenance; TAS.
CC GO: GO:0006832; P:small molecule transport; TAS.
CC InterPro: IPR002067; M:Mitocari.
CC InterPro: IPR002030; M:Uncoupling.
CC InterPro: IPR001993; M:Mitocari.
CC Pfam: PF00153; Mito-car; 3.
CC PRINTS: PR00926; MITOCARRIER.
CC PRINTS: PR00784; MTUNCOUPLING.
CC PROSITE: PS00215; MITOCH CARRIER. 3.
CC KM Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
CC KM Multigene family; Disease mutation.
CC FT TRANSMEM 12 29 1 (POTENTIAL).
CC FT TRANSMEM 73 91 2 (POTENTIAL).
CC FT TRANSMEM 117 134 3 (POTENTIAL).
CC FT TRANSMEM 176 195 4 (POTENTIAL).
CC FT TRANSMEM 214 231 5 (POTENTIAL).
CC FT TRANSMEM 273 291 6 (POTENTIAL).
CC FT REPEAT 1 110 1.
CC FT REPEAT 111 208 2.
CC FT REPEAT 209 298 3.
CC FT VARIANT 114 114 A -> P (IN PRO).
CC FT VARIANT 289 289 V -> M (IN PRO).
CC FT VARIANT 289 289 V -> A (IN PRO).
CC FT CONFLICT 147 149 G -> A (IN REF. 3).
CC FT CONFLICT 227 227 KGA -> R (IN REF. 3).
CC FT CONFLICT 227 227 V -> L (IN REF. 3).
CC SO SEQUENCE 298 AA; 33064 MW; 59F0DFAC4E7C9B CRC64;
Query Match 91.38; Score 1413; DB 1; Length 298;
Best Local Similarity 89.24; Pred. No. 6.9e-117;
Matches 265; Conservative 16; Mismatches 16; Indels 0; Gaps 0;

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QY 121 GAAGATSLCFVYPLDFARTRLAADVKGAREFERGLGDLVYKSDGKLYOGFNVS 180
DB 121 GAAGATSLCFVYPLDFARTRLAADVKGAREFERGLGDLVYKSDGKLYOGFNVS 180
QY 181 VGGIIIRAAVFECITOTAKGMDPKNTHTVISMIAQVYAVAGLTSPFDTVRRMMK 240
DB 181 VGGIIIRAAVFECITOTAKGMDPKNTHTVISMIAQVYAVAGLTSPFDTVRRMMK 240
QY 241 QSGRKGDIMYVTGLDCKWRKIADEGCAKFAFKKAWSNVLRGKGAVLYLYDEIKKY 297
DB 241 QSGRKGDIMYVTGLDCKWRKIADEGCAKFAFKKAWSNVLRGKGAVLYLYDEIKKY 297
RESULT 10
ADT_DROME STANDARD; PRT: 299 AA.
AC Q26365; P91614; Q26254; Q95530; Q9VZ70.
DT 15-JUL-1998 (Rel. 36, Created)
DT 28-FEB-2003 (Rel. 42, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE ADP/ATP carrier protein (ADP/ATP translocase) (adenine nucleotide
DE translocator) (ANT) (Stress sensitive B protein).
GN SRSB OR A/R-T OR CG16944.
OS Drosophila melanogaster (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID:7227;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-92389367; Pubmed-1387687;
RT Louvi A., Tsitilon S.G.;
RT "A cDNA clone encoding the ADP/ATP translocase of Drosophila
RT melanogaster shows a high degree of similarity with the mammalian
RT ADP/ATP translocases";
RL J. Mol. Evol. 35:44-50(1992).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE-94350065; Pubmed-7520869;
RT Hutter P., Karch F.;
RT "Molecular analysis of a candidate gene for the reproductive
RT isolation between sibling species of Drosophila.";
RL Experientia 50:749-762(1994).
RN [3]
RP SEQUENCE FROM N.A.
RX Zhang Y.Q., Davis A.W., Roote J., Herrmann S., Ashburner M.;
RT Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RC STRAIN-Berkeley;
RX MEDLINE-20196006; Pubmed-10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatidis P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers Y.-H.C., Blazer R.G., Champe M., Pfeiffer B.D.,
RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA Abriel J.F., Abdoyani A., An H.-J., Andrews-Pfankoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Bertman B.P., Bhandari D., Bolshakov S.,
RA Borokova D., Botchan M.R., Bouck J., Brokstein P., Brotler P.,
RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferrieres S., Fleischmann W.,
RA Foster C., Gabrielian A.E., Gary N.S., Gelbart W.M., Glasser K.,
RA Gload A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Idegami C.,
RA Jaitani M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

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DR PRINTS: PR00926; MITOCHARRIER.
DR PROSITE: PS00215; MITOCH_CARRIER; 2.
KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
KW Transf. peptide; Multigene family.
FT TRANSIT 1 76 MITOCHONDRION (BY SIMILARITY).
FT CHAIN 77 386 ADP/ATP CARRIER PROTEIN 1.
FT TRANSMEM 90 107 1 (POTENTIAL).
FT TRANSMEM 152 170 2 (POTENTIAL).
FT TRANSMEM 195 212 3 (POTENTIAL).
FT TRANSMEM 256 275 4 (POTENTIAL).
FT TRANSMEM 295 312 5 (POTENTIAL).
FT TRANSMEM 351 369 6 (POTENTIAL).
SO SEQUENCE 386 AA; 42093 MW; A05F6C73EEDEE6 CRC64;

Query Match 49.8%; Score 771; DB 1; Length 386;
Best Local Similarity 55.4%; Pred. No. 2.3e-60;
Matches 169; Conservative 35; Mismatches 79; Indels 22; Gaps 7;

OY 7 SPANFLAGVAAAIKTAAPIERKLLQVQ-HASKQITADKQYGIIDCVRIPEQ 65
DB 85 SFADIFLMGVSAAVSKTAAPIERKLLIONODEMIRSGRLSEYKIGICDFKRTIDE 144
OY 66 EVLSFWRGNTLVNRYPTQALNFAKDKYKQIFLGVDKRTQFWRYFAGNLASGAGA 125
DB 145 GFGLMRGNTLVNRYPTQALNFAKDKYKQIFLGVDKRTQFWRYFAGNLASGAGA 203
OY 126 TSLCFVYPLDPAFARLADV--VGRAGAEFEREGDGLVLYKSDIGLGYGFVNVSYG 183
DB 204 SSLFVYSLDYARLRANDAKAKKGERQNGLVDRYKRLKSGINGLVGFNISCVG 263
OY 184 IITRAAYFGIYDPAK-----GMLPDPKNTLVISWMTAQVTVAVAGLTSPEFTVRRM 238
DB 264 IIVRGLEFGMDSLKPVLTGSMDSFFASFLVGLMLT---TNCALALASYPIDVRRRM 319
OY 239 MMOSGRKTDIMYGTGLCMRKIRANDEGKAFEGGAWNVLRGMAFVLYVYDEI--- 294
DB 320 MMTSGKA---VKYSSLDPAFSGIILNKGKSLFKGAGSNILNALAGVAGLYDKQLTIV 376
OY 295 --KKY 297
DB 377 FGKKY 381

RESULT 14
ADT_SCHPO STANDARD: PRT: 322 AA.
AC 009188:
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE ADP/ATP carrier protein (ADP/ATP translocase) (Adenine nucleotide translocator) (ANT).
GN ANCI OR SPBC530.10C.
OS Schizosaccharomyces pombe (Fission yeast).
OC Eukaryota; Fungi; Ascomycota; Schizosaccharomycetes; Schizosaccharomycetaceae; Schizosaccharomycetaceae; Schizosaccharomycetes.
OC Schizosaccharomycetes.
OX NCBI_TaxID=4896;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=96257204; PubMed=8675018;
RA Couzin N., Trezeguet V., Sauc A.L., Lauguin G.J.M.;
RT Cloning of the gene encoding the mitochondrial adenine nucleotide carrier of Schizosaccharomyces pombe by functional complementation in Saccharomyces cerevisiae.
RL Gene 171:113-117(1996).
RP SEQUENCE FROM N.A.
RC STRAIN=972;
RX MEDLINE=21848401; PubMed=11859360;
RA Wood V., Williams R., Rajandream M.A., Lyne M., Lyne R., Stewart A., Sgouras J., Peat N., Hayles J., Baker S., Basham D., Bowman S.,

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RA Brooks K., Brown D., Brown S., Chillingworth T., Churcher C.M.,
RA Collins M., Connor R., Cronin A., Davis P., Fellwell T., Fraser A.,
RA Gellens S., Goble A., Hamlin N., Harris D., Hildago J., Hodgson G.,
RA Holroyd S., Hornby T., Howarth S., Huckle E.J., Hunt S., Jagsels K.,
RA James K., Jones L., Jones M., Leather S., McDonald S., McLean J.,
RA Mooney P., Moule S., Mungall K., Murphy U., Niblett D., Odeil C.,
RA Oliver K., O'Neill S., Pearson D., Quail M.A., Rabbitts E.,
RA Rutherford K., Rutter S., Saunders D., Seeger K., Sharp S.,
RA Skellton J., Simmonds M., Squares R., Squares S., Stevens K.,
RA Taylor K., Taylor R.G., Tivey A., Walsh S.V., Warren T., Whitehead S.,
RA Woodward J., Volckaert G., Aert R., Robben J., Grynoprez B.,
RA Weljens I., Vanstreels E., Rieger M., Schaefer M., Mueller-Auer S.,
RA Gabel C., Fuchs M., Fritzc C., Holzer E., Moestl D., Hilbert H.,
RA Borzym K., Langer I., Beck A., Lehnach H., Reinhardt R., Pohl T.M.,
RA Eger P., Zimmermann W., Medler H., Mandut R., Purrelle B.,
RA Goffeau A., Cadieu E., Dreano S., Gloux S., Lelaure V., Mottier S.,
RA Galbert F., Aves S.J., Xiang Z., Hunt C., Moore K., Hurst S.M.,
RA Lucas M., Rochet M., Galliard C., Talida V.A., Garzon A., Thode G.,
RA Daga R.R., Cruzado L., Jimenez J., Sanchez M., del Rey F., Benito J.,
RA Dominguez A., Revuelta J.L., Moreno S., Armstrong J., Forsburg S.L.,
RA Cerutti L., Lowe T., McCombie M.R., Paulsen I., Potashkin J.,
RA Shpakovski G.V., Ussery D., Barrett B.G., Nurse P.;
RA "The genome sequence of Schizosaccharomyces pombe."
RT Nature 415:871-880(2002).
CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE MITOCHONDRIAL INNER MEMBRANE.
CC -1- SUBUNIT: Homodimer (By similarity).
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial inner membrane.
CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
CC This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation - the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/ or send an email to license@isb-sib.ch).
CC EMBL: 249974; CA90275.1; -.
CC EMBL: AL023634; CA91976.1; -.
CC PIR: T40526; T40526.
CC GeneDB: SPombe; SPBC530.10C; -.
CC InterPro: IPR002067; Mit_carrier.
CC InterPro: IPR001993; Mitoch_carrier.
CC Pfam: PR00926; Mitoch_carrier; 3.
CC PRINTS: PR00926; MITOCHARRIER.
DR PROSITE: PS00215; MITOCH_CARRIER; 2.
KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport.
FT TRANSMEM 28 48 1 (POTENTIAL).
FT TRANSMEM 93 111 2 (POTENTIAL).
FT TRANSMEM 131 151 3 (POTENTIAL).
FT TRANSMEM 197 217 4 (POTENTIAL).
FT TRANSMEM 242 262 5 (POTENTIAL).
FT TRANSMEM 289 309 6 (POTENTIAL).
SO SEQUENCE 322 AA; 35020 MW; 8AC3D16A0F41AFC CRC64;

Query Match 49.8%; Score 770; DB 1; Length 322;
Best Local Similarity 53.6%; Pred. No. 2.3e-60;
Matches 158; Conservative 51; Mismatches 74; Indels 12; Gaps 6;

OY 7 SPANFLAGVAAAIKTAAPIERKLLQVQ-HASKQITADKQYGIIDCVRIPEK 63
DB 26 TFFPDMGVSAAVSKTAAPIERKLLION--DEMIRAGLSIRYKIGICDFKRTIA 83
OY 64 EVLSFWRGNTLVNRYPTQALNFAKDKYKQIFLGVDKRTQFWRYFAGNLASGAGA 123
DB 84 EGVLSFWRGNTLVNRYPTQALNFAKDKYKQIFLGVDKRTQFWRYFAGNLASGAGA 142
OY 124 GATSLCFVYPLDPAFARLADV--VGRAGAEFEREGDGLVLYKSDIGLGYGFVNVSY 181
DB 143 GASLLEFVSLDYARLRANDAKAKKGERQNGLVDRYKRLKSGINGLVGFNISCVG 202

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Db      121 GAAGATSLCFVYPLDFAKRLADVGKAGEREFGDGLVITVSDGRLGTYQGNVS 180
QY      181 VGGIITIRAAVFGIYDTAKGMLPDPKNTHTIVISMTAQVTAVAGLTSYFPTVRRMM 240
      181 VGGIITIRAAVFGIYDTAKGMLPDPKNTHTIVISMTAQVTAVAGLTSYFPTVRRMM 240
Db      241 QSGRKGTDIMYTGTLDCWKRIADDEGKAFKFGKAMSNVLRGMCAPVLVLYDEIKRY 298
      241 QSGRKGTDIMYTGTLDCWKRIADDEGKAFKFGKAMSNVLRGMCAPVLVLYDEIKRY 298

RESULT 2
O9PRH1  PRELIMINARY; PRT; 298 AA.
ID      O9RH10
AC      O9RH10;
DT      01-OCT-2002 (TREMBLrel. 22, Created)
DT      01-OCT-2002 (TREMBLrel. 22, Last sequence update)
DE      01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE      Solute carrier family 25 member 5 protein.
GN      SLC35A5.
OS      Brachydanio rerio (zebrafish) (Danio rerio).
OC      Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC      Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
OC      Cyprinidae; Danio.
OX      NCBI_TaxID=7955;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=22035902; PubMed=12006978;
RA      Gollig G., Amsterdam A., Sun Z., Antonelli M., Maldonado E., Chen W.,
RA      Burgess S., Haldt M., Artzt K., Farrington S., Lin S.-Y., Nissen R.M.,
RA      Hopkins N.;
RT      Interlational mutagenesis in zebrafish rapidly identifies genes
RT      essential for early vertebrate development.
RL      Nat. Genet. 31:135-140(2002).
DR      EMBL: AF506216; AAM34660.1;
DR      InterPro: IPR001993; Mitoch_carrier.
DR      InterPro: IPR002067; Mit_carrier.
DR      InterPro: IPR002030; Mit_uncoupling.
DR      Pfam: PF00153; mito_car1; 3.
DR      PRINTS: PR00926; MITOCARRIER.
DR      PRINTS: PR00784; MTUNCOUPLING.
DR      PROSITE: PS00215; MITOCH_CARRIER.
DR      PROSITE: PS00215; MITOCH_CARRIER; 3.
SQ      SEQUENCE 298 AA; 32763 MW; D78663CF65C51D39 CRC64;

Query Match      93.7%; Score 1450; DB 13; Length 298;
Best Local Similarity 92.9%; Pred. No. 3e-120;
Matches 275; Conservative 13; Mismatches 8; Indels 0; Gaps 0;

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AC      Q9PRH1;
DT      01-MAY-2000 (TREMBLrel. 13, Created)
DT      01-MAY-2000 (TREMBLrel. 13, Last sequence update)
DT      01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE      ADP/ATP translocase.
OS      Rana rugosa (winkled frog).
OC      Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC      Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Rana.
OX      NCBI_TaxID=8410;
RN      [1]
RP      SEQUENCE FROM N.A.
RX      MEDLINE=99083429; PubMed=9866197;
RA      Miura I., Ontani H., Nakamura M., Ichikawa Y., Satoh K.;
RT      The origin and differentiation of the heteromorphic sex chromosomes
RT      Z, W, X, and Y in the frog Rana rugosa. Inferred from the sequences of
RT      a sex-linked gene, ADP/ATP translocase.
RL      Mol. Biol. Evol. 15:1612-1619(1998).
CC      -1-SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
DR      EMBL: AB008463; BAA36513.1;
DR      EMBL: AB008456; BAA36506.1;
DR      EMBL: AB008461; BAA36511.1;
DR      EMBL: AB008462; BAA36512.1;
DR      InterPro: IPR001993; Mitoch_carrier.
DR      InterPro: IPR002067; Mit_carrier.
DR      InterPro: IPR002030; Mit_uncoupling.
DR      Pfam: PF00153; mito_car1; 3.
DR      PRINTS: PR00926; MITOCARRIER.
DR      PRINTS: PR00784; MTUNCOUPLING.
DR      PROSITE: PS00215; MITOCH_CARRIER.
DR      PROSITE: PS00215; MITOCH_CARRIER; 3.
KW      Membrane; Transmembrane; Transport.
SQ      SEQUENCE 298 AA; 33054 MW; B0E23AD56F548D36 CRC64;

Query Match      93.5%; Score 1446; DB 13; Length 298;
Best Local Similarity 91.9%; Pred. No. 6.8e-120;
Matches 273; Conservative 14; Mismatches 10; Indels 0; Gaps 0;

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"The origin and differentiation of the heteromorphic sex chromosomes of 2, w, x, and y in the frog Rana rugosa, inferred from the sequences of a sex-linked gene, ADP/ATP translocase.";
 RL Mol. Biol. Evol. 15:1612-1619(1998).
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
 DR EMBL: AB008460; BAA36510.1; -;
 DR EMBL: AB008458; BAA36508.1; -;
 DR EMBL: AB008459; BAA36509.1; -;
 DR InterPro: IPR001993; Mitoch_carrier.
 DR InterPro: IPR002067; Mit_carrier.
 DR InterPro: IPR002030; Mit_uncoupling.
 DR Pfam: PF00153; mito_carr; 3.
 DR PRINTS: PR00926; MITOCARRIER.
 DR PROSITE: PS00784; MTUNCOUPLING.
 DR PROSITE: PS00215; MITOCH_CARRIER; 3.
 KW Membrane; Transmembrane; Transport.
 SQ SEQUENCE 298 AA; 33082 MW; BOE225E867599A06 CRC64;

Query Match 93.3%; Score 1443; DB 13; Length 298;
 Best Local Similarity 91.6%; Pred. No. 1.2e-119;
 Matches 272; Conservative 15; Mismatches 10; Indels 0; Gaps 0;

OY 1 MTDALSPAKDFLAGVAAAIKTAIVAPIERVKLLIQVHASKOTADKQYKGIIDCYVR 60
 DB 1 MTDALSPAKDFLAGVAAAIKTAIVAPIERVKLLIQVHASKOTADKQYKGIIDCYVR 60
 OY 61 IPKEQVLSFWRGNTLVNRYPTQALNFAFKDKYKQIFLGVDKRTQFMRYFAGNLASG 120
 DB 61 IPKEQVLSFWRGNTLVNRYPTQALNFAFKDKYKQIFLGVDKRTQFMRYFAGNLASG 120
 OY 61 IPKEQVLSFWRGNTLVNRYPTQALNFAFKDKYKQIFLGVDKRTQFMRYFAGNLASG 120
 DB 61 IPKEQVLSFWRGNTLVNRYPTQALNFAFKDKYKQIFLGVDKRTQFMRYFAGNLASG 120
 OY 121 GAAGATSLCFEYPLDFARTRLADYGVKAGAREFERGLDCLVKIKYKSDGKGLYOGFNVS 180
 DB 121 GAAGATSLCFEYPLDFARTRLADYGVKAGAREFERGLDCLVKIKYKSDGKGLYOGFNVS 180
 OY 121 GAAGATSLCFEYPLDFARTRLADYGVKAGAREFERGLDCLVKIKYKSDGKGLYOGFNVS 180
 DB 121 GAAGATSLCFEYPLDFARTRLADYGVKAGAREFERGLDCLVKIKYKSDGKGLYOGFNVS 180
 OY 181 VGGIITVRAAYFGIYDTAKGMLPDPKNTHTVISMIAQTVAVAGILSTYPTVRRMM 240
 DB 181 VGGIITVRAAYFGIYDTAKGMLPDPKNTHTVISMIAQTVAVAGILSTYPTVRRMM 240
 OY 241 QSGRKGTDIMYTGIDCWKRKTARDEGSKAFKFGAMSNVLRGMAFVLYLDEIKKY 297
 DB 241 QSGRKGTDIMYTGIDCWKRKTARDEGSKAFKFGAMSNVLRGMAFVLYLDEIKKY 297
 RESULT 5
 OY 08AYM3 PRELIMINARY; PRT; 298 AA.
 AC 08AYM3:
 DT 01-MAR-2003 (TREMBlrel. 23, Created)
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE ATP/ADP antiporter.
 GN AVANT.
 OS Gallus gallus (Chicken).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
 CC Gallus.
 CC NCBI_TaxID=9031;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Toyomizu M., Ueda M., Sato S., Seki Y., Sato K., Akiba Y.;
 RT "Cold-induced mitochondrial uncoupling and expression of chicken UCP
 RT and ANT mRNA in chicken skeletal muscle.";
 RL FEBS Lett. 0:0-0(2002).
 DR EMBL: AB008686; BAC15533.1; -;
 SQ SEQUENCE 298 AA; 32847 MW; 1174CC5EC400A10D CRC64;

Query Match 93.3%; Score 1443; DB 13; Length 298;
 Best Local Similarity 92.9%; Pred. No. 1.2e-119;
 Matches 275; Conservative 9; Mismatches 12; Indels 0; Gaps 0;

OY 1 MTDALSPAKDFLAGVAAAIKTAIVAPIERVKLLIQVHASKOTADKQYKGIIDCYVR 60
 DB 1 MTDALSPAKDFLAGVAAAIKTAIVAPIERVKLLIQVHASKOTADKQYKGIIDCYVR 60

OY 61 IPKEQVLSFWRGNTLVNRYPTQALNFAFKDKYKQIFLGVDKRTQFMRYFAGNLASG 120
 DB 61 IPKEQVLSFWRGNTLVNRYPTQALNFAFKDKYKQIFLGVDKRTQFMRYFAGNLASG 120
 OY 121 GAAGATSLCFEYPLDFARTRLADYGVKAGAREFERGLDCLVKIKYKSDGKGLYOGFNVS 180
 DB 121 GAAGATSLCFEYPLDFARTRLADYGVKAGAREFERGLDCLVKIKYKSDGKGLYOGFNVS 180
 OY 121 GAAGATSLCFEYPLDFARTRLADYGVKAGAREFERGLDCLVKIKYKSDGKGLYOGFNVS 180
 DB 121 GAAGATSLCFEYPLDFARTRLADYGVKAGAREFERGLDCLVKIKYKSDGKGLYOGFNVS 180
 OY 181 VGGIITVRAAYFGIYDTAKGMLPDPKNTHTVISMIAQTVAVAGILSTYPTVRRMM 240
 DB 181 VGGIITVRAAYFGIYDTAKGMLPDPKNTHTVISMIAQTVAVAGILSTYPTVRRMM 240
 OY 241 QSGRKGTDIMYTGIDCWKRKTARDEGSKAFKFGAMSNVLRGMAFVLYLDEIKKY 296
 DB 241 QSGRKGTDIMYTGIDCWKRKTARDEGSKAFKFGAMSNVLRGMAFVLYLDEIKKY 296

RESULT 6
 OY 09YIC4 PRELIMINARY; PRT; 298 AA.
 ID 09YIC4:
 AC 09YIC4:
 DT 01-MAY-1999 (TREMBlrel. 10, Created)
 DT 01-MAY-1999 (TREMBlrel. 10, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE ADP/ATP translocase.
 OS Rana rugosa (Fringed frog).
 CC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 CC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
 CC NCBI_TaxID=8410;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA MEDLINE-99083429; PubMed-9866197;
 RA Miura I., Ohtani H., Nakamura M., Ichikawa Y., Satoh K.;
 RT "The origin and differentiation of the heteromorphic sex chromosomes
 RT of 2, w, x, and y in the frog Rana rugosa, inferred from the sequences of
 RT a sex-linked gene, ADP/ATP translocase.";
 RL Mol. Biol. Evol. 15:1612-1619(1998).
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
 DR EMBL: AB008457; BAA36507.1; -;
 DR InterPro: IPR001993; Mitoch_carrier.
 DR InterPro: IPR002067; Mit_carrier.
 DR InterPro: IPR002030; Mit_uncoupling.
 DR Pfam: PF00153; mito_carr; 3.
 DR PRINTS: PR00926; MITOCARRIER.
 DR PRINTS: PR00784; MTUNCOUPLING.
 DR PROSITE: PS00215; MITOCH_CARRIER; 3.
 KW Membrane; Transmembrane; Transport.
 SQ SEQUENCE 298 AA; 33068 MW; 15B270ED37099A00 CRC64;

Query Match 93.0%; Score 1439; DB 13; Length 298;
 Best Local Similarity 91.2%; Pred. No. 2.8e-119;
 Matches 271; Conservative 16; Mismatches 10; Indels 0; Gaps 0;

OY 1 MTDALSPAKDFLAGVAAAIKTAIVAPIERVKLLIQVHASKOTADKQYKGIIDCYVR 60
 DB 1 MTDALSPAKDFLAGVAAAIKTAIVAPIERVKLLIQVHASKOTADKQYKGIIDCYVR 60
 OY 61 IPKEQVLSFWRGNTLVNRYPTQALNFAFKDKYKQIFLGVDKRTQFMRYFAGNLASG 120
 DB 61 IPKEQVLSFWRGNTLVNRYPTQALNFAFKDKYKQIFLGVDKRTQFMRYFAGNLASG 120
 OY 121 GAAGATSLCFEYPLDFARTRLADYGVKAGAREFERGLDCLVKIKYKSDGKGLYOGFNVS 180
 DB 121 GAAGATSLCFEYPLDFARTRLADYGVKAGAREFERGLDCLVKIKYKSDGKGLYOGFNVS 180
 OY 121 GAAGATSLCFEYPLDFARTRLADYGVKAGAREFERGLDCLVKIKYKSDGKGLYOGFNVS 180
 DB 121 GAAGATSLCFEYPLDFARTRLADYGVKAGAREFERGLDCLVKIKYKSDGKGLYOGFNVS 180
 OY 181 VGGIITVRAAYFGIYDTAKGMLPDPKNTHTVISMIAQTVAVAGILSTYPTVRRMM 240
 DB 181 VGGIITVRAAYFGIYDTAKGMLPDPKNTHTVISMIAQTVAVAGILSTYPTVRRMM 240
 OY 241 QSGRKGTDIMYTGIDCWKRKTARDEGSKAFKFGAMSNVLRGMAFVLYLDEIKKY 297
 DB 241 QSGRKGTDIMYTGIDCWKRKTARDEGSKAFKFGAMSNVLRGMAFVLYLDEIKKY 297

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RESULT 7
ID 0919M9 PRELIMINARY; PRT; 298 AA.
AC 0919M9;
DT 01-OCT-2000 (TEMBLrel. 15, Created)
DT 01-OCT-2000 (TEMBLrel. 15, Last sequence update)
DT 01-MAR-2003 (TEMBLrel. 23, Last annotation update)
DE Adenine nucleotide translocase.
GN ANTI.
OS Xenopus laevis (African clawed frog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Amphibia; Batrachia; Anura; Mesobatrachia; Pipridae; Pipidae;
OC Xenopodinae; Xenopus.
OX NCBI_TaxID=8355;
RN [1]
RP SEQUENCE FROM N.A.
RA Crawford M.J., Khosrovshanian F., Varmuza S.L., Liversage R.A.;
RT "Xenopus Adenine Nucleotide Translocase mRNA Exhibits Specific and
RT Dynamic Patterns of Expression During Development.";
RL Submitted (FEB-2000) to the EMBL/GenBank/DBJ databases.
CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
DR EMBL: AF23147; AAF63471.1;
DR InterPro: IPR001993; Mitoch_carrier.
DR InterPro: IPR002067; Mlt_carrier.
DR Pfam: PF00153; Mito_carr; 3.
DR PRINTS: PR00926; MITOCARRIER.
DR PROSITE: PS00784; MTUNCOUPLING.
DR MEMBRANE: TRANSMEMBRANE; TRANSPORT.
KW KMW.
SQ SEQUENCE 298 AA; 32940 MW; 91B/40133751877E CRC64;

Query Match 92.1%; Score 1425; DB 13; Length 298;
Best local Similarity 91.6%; Pred. No. 4,9e-118;
Matches 271; Conservative 11; Mismatches 14; Indels 0; Gaps 0;

QY 1 MTDALSPAKDPLAGVAAAIKSTVAAPIERVKLLQVQHASQITADKQYKGIIDCVR 60
DB 1 MTDALSPAKDPLAGVAAAIKSTVAAPIERVKLLQVQHASQITADKQYKGIIDCVR 60
QY 61 IPKEQVLSFWRGNLANVIRYPTQALNFAFKDKYKQIFGVDKRTQFRYFAGNLASG 120
DB 61 IPKEQVLSFWRGNLANVIRYPTQALNFAFKDKYKQIFGVDKRTQFRYFAGNLASG 120
QY 121 GAAGATSLCFVYPLDFARTLADVGAAGAREFRGIGDCLVITYSDGKIGLYOGFNVS 180
DB 121 GAAGATSLCFVYPLDFARTLADVGAAGAREFRGIGDCLVITYSDGKIGLYOGFNVS 180
QY 181 VGGIIIRAAVFGIYDTAKMPLDPKNTHTIVSMIAQVTAAGLSTYFDTVRRRMM 240
DB 181 VGGIIIRAAVFGIYDTAKMPLDPKNTHTIVSMIAQVTAAGLSTYFDTVRRRMM 240
QY 241 OSGRKGDIMYTGTLDCWRKIARDEGKAFKGAWSNVLRGMAFVLVYDEIKK 296
DB 241 OSGRKGDIMYTGTLDCWRKIARDEGKAFKGAWSNVLRGMAFVLVYDEIKK 296
DB 241 OSGRKGDIMYTGTLDCWRKIARDEGKAFKGAWSNVLRGMAFVLVYDEIKK 296

RESULT 8
ID 046373 PRELIMINARY; PRT; 298 AA.
AC 046373;
DT 01-JUN-1998 (TEMBLrel. 06, Created)
DT 01-JUN-1998 (TEMBLrel. 06, Last sequence update)
DT 01-MAR-2003 (TEMBLrel. 23, Last annotation update)
DE ADP/ATP translocase.
OS Oryctolagus cuniculus (Rabbit).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
OX NCBI_TaxID=9986;
RN [1]
RP SEQUENCE FROM N.A.

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RC TISSUE=Skeletal muscle;
RA Yamaguchi N., Kasai M.;
RT "Identification of a 30kDa calsequestrin-binding protein, which
RT regulates calcium release from sarcoplasmic reticulum of rabbit
RT skeletal muscle.";
RL J. Biochem. 335:541-547(1998).
CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
DR EMBL: AB009386; BAA23777.1;
DR InterPro: IPR001993; Mitoch_carrier.
DR InterPro: IPR002067; Mlt_carrier.
DR InterPro: IPR002030; Mlt_uncoupling.
DR Pfam: PF00153; Mito_carr; 3.
DR PRINTS: PR00926; MITOCARRIER.
DR PROSITE: PS00784; MTUNCOUPLING.
DR KMW.
KW Membrane; Transmembrane; Transport.
SQ SEQUENCE 298 AA; 32901 MW; CAEA32C88164AD78 CRC64;

Query Match 92.0%; Score 1423; DB 6; Length 298;
Best local Similarity 89.9%; Pred. No. 7,4e-118;
Matches 267; Conservative 16; Mismatches 14; Indels 0; Gaps 0;

QY 1 MTDALSPAKDPLAGVAAAIKSTVAAPIERVKLLQVQHASQITADKQYKGIIDCVR 60
DB 1 MSDQALSLKDFLAGVAAAVSTVAAPIERVKLLQVQHASQITADKQYKGIIDCVR 60
QY 61 IPKEQVLSFWRGNLANVIRYPTQALNFAFKDKYKQIFGVDKRTQFRYFAGNLASG 120
DB 61 IPKEQVLSFWRGNLANVIRYPTQALNFAFKDKYKQIFGVDKRTQFRYFAGNLASG 120
QY 121 GAAGATSLCFVYPLDFARTLADVGAAGAREFRGIGDCLVITYSDGKIGLYOGFNVS 180
DB 121 GAAGATSLCFVYPLDFARTLADVGAAGAREFRGIGDCLVITYSDGKIGLYOGFNVS 180
QY 181 VGGIIIRAAVFGIYDTAKMPLDPKNTHTIVSMIAQVTAAGLSTYFDTVRRRMM 240
DB 181 VGGIIIRAAVFGIYDTAKMPLDPKNTHTIVSMIAQVTAAGLSTYFDTVRRRMM 240
QY 241 OSGRKGDIMYTGTLDCWRKIARDEGKAFKGAWSNVLRGMAFVLVYDEIKK 297
DB 241 OSGRKGDIMYTGTLDCWRKIARDEGKAFKGAWSNVLRGMAFVLVYDEIKK 297

RESULT 9
ID 08BV19 PRELIMINARY; PRT; 298 AA.
AC 08BV19;
DT 01-MAR-2003 (TEMBLrel. 23, Created)
DT 01-MAR-2003 (TEMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TEMBLrel. 23, Last annotation update)
DE Solute carrier family 25.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sclurognath; Muridae; Murinae; Mus.
OX NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RA STRAIN=C57BL/6J; TISSUE=Medulla oblongata;
RA MEDLINE=22354683; Pubmed=1246851;
RA THE FANTOM CONSORTIUM.
RA THE RIKEN GENOME EXPLORATION RESEARCH GROUP PHASE I & II TEAM;
RT "Analysis of the mouse transcriptome based on functional annotation of
RT Nature 420:563-573(2002).
DR EMBL: AK078077; BAC37117.1;
SQ SEQUENCE 298 AA; 32904 MW; F94C89009836710B CRC64;

Query Match 91.6%; Score 1417; DB 11; Length 298;
Best local Similarity 89.6%; Pred. No. 2,5e-117;
Matches 266; Conservative 15; Mismatches 16; Indels 0; Gaps 0;

QY 1 MTDALSPAKDPLAGVAAAIKSTVAAPIERVKLLQVQHASQITADKQYKGIIDCVR 60
DB 1 MTDALSPAKDPLAGVAAAIKSTVAAPIERVKLLQVQHASQITADKQYKGIIDCVR 60

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Db      1 MGDALSLKDFLAGGIAAASKTAADPIERVKLLLOVHASKQISAEKQYKGIIDCVVR 60
Oy      61 IPKEQVLSFWRGNLANVIRYFPTQALNFAFKDKYQIFLGVDKRTQFWRFPAGNLASG 120
        ||||| :|||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      61 IPKQGLSFWRGNIANVIRYFPTQALNFAFKDKYQIFLGVDKRTQFWRFPAGNLASG 120
Oy      121 GAAGATSLCFYVPLDFARTRLAADYGKAGAEERFGLDCLVTKYKSDGIKGLYGFNV 180
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      121 GAAGATSLCFYVPLDFARTRLAADYGKAGAEERFGLDCLVTKYKSDGIKGLYGFNV 180
Oy      181 VOGIITVAAAFGYVDTAKGMLPDKNTHIVISWMIAGQVTVAVAGLTSYPTVRRMM 240
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      181 VOGIITVAAAFGYVDTAKGMLPDKNTHIVISWMIAGQVTVAVAGLTSYPTVRRMM 240
Oy      241 OSGRKGTDMYTGTLDCWKRIARDEGKAFKAGSNVLRGNGAFVLYLDEIKY 297
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      241 OSGRKGTDMYTGTLDCWKRIARDEGKAFKAGSNVLRGNGAFVLYLDEIKY 297

RESULT 10
Oy      091336 PRELIMINARY: PRT: 317 AA.
AC      091336:
DT      01-NOV-1996 (TREMBLrel. 01, Created)
DT      01-MAY-1999 (TREMBLrel. 10, Last sequence update)
DT      01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE      ADP/ATP translocase.
OS      Rana sylvatica (Wood frog).
OC      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC      Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Ranidae; Rana.
OX      NCBI_TaxID=43438;
RN      [1]
RP      SEQUENCE FROM N.A.
RC      TISSUE-Liver;
RX      MEDLINE=97398141; PubMed=9256066;
RA      Cal O., Greenway S.C., Storey K.B.;
RT      Differential regulation of the mitochondrial ADP/ATP translocase gene
RT      in wood frogs under freezing stress.*;
RL      Blochm. Biophys. Acta 1353:69-78(1997).
RN      [2]
RP      SEQUENCE FROM N.A.
RC      TISSUE-Liver;
RA      Cal O., Storey K.B.;
RL      Submitted (Apr-1999) to the EMBL/GenBank/DBJ databases.
CC      -1. SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
DR      EMBL: U44832; AAA97882.2; -.
DR      InterPro: IPR001993; Mitoch.carrier.
DR      InterPro: IPR002067; Mit.carrier.
DR      Pfam: PF00153; mito_car; 3.
DR      PRINTS: PR00926; MITOCARRIER.
DR      PROSITE: PS00215; MITOCH_CARRIER; 3.
KW      Membrane; Transmembrane; Transport.
SQ      SEQUENCE 317 AA; 35005 MW; 5f66b7bd8d5ceb72 CRC64;

Query Match      83.7%; Score 1295; DB 13; Length 317;
Best Local Similarity 90.1%; Pred. No. 1.7e-106;
Matches 245; Conservative 14; Mismatches 13; Indels 0; Gaps 0;

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Oy      241 OSGRKGTDMYTGTLDCWKRIARDEGKAFK 272
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      241 OSGRKGTDMYTGTLDCWKRIARDEGKAFK 272

RESULT 11
Oy      095VX4 PRELIMINARY: PRT: 299 AA.
AC      095VX4:
DT      01-DEC-2001 (TREMBLrel. 19, Created)
DT      01-DEC-2001 (TREMBLrel. 19, Last sequence update)
DT      01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE      ADP-ATP translocator.
OS      Ethmostigmus rubripes.
OC      Eukaryota; Metazoa; Arthropoda; Myriapoda; Chilopoda;
OC      Pleurostigmophora; Scolopendromorpha; Scolopendridae; Ethmostigmus.
OX      NCBI_TaxID=62613;
RN      [1]
RP      SEQUENCE FROM N.A.
RA      Burrell J.N.;
RT      "Nucleotide sequence of an ADP-ATP translocator of Ethmostigmus
RT      rubripes."
RL      Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
DR      EMBL: AF401758; AAL02100.1; -.
DR      InterPro: IPR001993; Mitoch.carrier.
DR      InterPro: IPR002067; Mit.carrier.
DR      Pfam: PF00153; mito_car; 3.
DR      PRINTS: PR00926; MITOCARRIER.
DR      PROSITE: PS00215; MITOCH_CARRIER; 3.
SQ      SEQUENCE 299 AA; 33037 MW; 3c3bbcb26e7c3c5e CRC64;

Query Match      82.6%; Score 1278; DB 5; Length 299;
Best Local Similarity 82.8%; Pred. No. 5.2e-105;
Matches 241; Conservative 22; Mismatches 28; Indels 0; Gaps 0;

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Oy      5 ALSFAKDFLAGGVAIAISKTAVAPIERVLLLOVHASKQITADKQYKGIIDCVVRIPKE 64
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      5 AVSFLKDFLAGGVAIAISKTAVAPIERVLLLOVHASKQIADVQYKGMVDCFRVIRPGE 64
Oy      65 QEVLSFWRGNLANVIRYFPTQALNFAFKDKYQIFLGVDKRTQFWRFPAGNLASGGAAG 124
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      65 QGILSYWRGNLANVIRYFPTQALNFAFKDKYQIFLGVDKRTQFWRFPAGNLASGGAAG 124
Oy      125 ATSLCFVYPLDFARTRLAADYGKAGAEERFGLDCLVTKYKSDGIKGLYGFNVSYOGI 184
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      125 ATSLCFVYPLDFARTRLAADYGKAGAEERFGLDCLVTKYKSDGIKGLYGFNVSYOGI 184
Oy      185 IYRAAYFGYVDTAKGMLPDKNTHIVISWMIAGQVTVAVAGLTSYPTVRRMMQSGR 244
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      185 IYRAAYFGYVDTAKGMLPDKNTHIVISWMIAGQVTVAVAGLTSYPTVRRMMQSGR 244
Oy      245 KGTDMYTGTLDCWKRIARDEGKAFKAGSNVLRGNGAFVLYLDEIK 295
        |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db      245 KRADILYKNTIDCWGRIYTBEGAAFFKAGAFSNILGTGAGAVLYLDEIK 295

RESULT 12
Oy      081RA0 PRELIMINARY: PRT: 312 AA.
AC      081RA0:
DT      01-MAR-2003 (TREMBLrel. 23, Created)
DT      01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT      01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE      CG16944-PC.
GN      SESB.
OS      Drosophila melanogaster (Fruit fly).
OC      Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC      Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC      Ephydroidea; Drosophilidae; Drosophila.
OX      NCBI_TaxID=7227;
RN      [1]
RP      SEQUENCE FROM N.A.

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RA MEDLINE-20196006; PubMed-10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Mortman J.R., Vandeil M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.H., Bialek R.G., Chame M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gaber G.L.,
 RA Abrell J.F., Agbayan A., An H.J., Andrews-Pfannkuch C., Baldwin D.,
 RA Baller R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borikova D., Busam D.A., Bouck J., Brokstein P., Brothier P.,
 RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Fouts R., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwan C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Jimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lascko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Mlshina N.V., Mobarry C., Morris J., Moshrefi A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nuskern D.R., Paclel J.M.,
 RA Palazolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.Y., Wasserman D.A., Weislock G.M., Weissenbach J.,
 RA Williams S.M., Woodagert, Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
 RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao X., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RA "The genome sequence of Drosophila melanogaster.";
 RA Science 287:2185-2195(2000).
 RA [2]
 RA SEQUENCE FROM N.A.
 RA Celniker S.E., Adams M.D., Krommiller B., Wan K.H., Holt R.A.,
 RA Evans C.A., Gocayne J.D., Amanatides P.G., Brandon R.C., Rogers Y.,
 RA Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,
 RA Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
 RA Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,
 RA Ferreira S., Frise E., Galle R.F., Garg N.S., George R.A.,
 RA Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
 RA Ibegwan C., Jalali M., Kruse D., Li P., Mattei B., Moshrefi A.,
 RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunco J.,
 RA Paclel J., Paragas V., Park S., Patel S., Pfeiffer B.,
 RA Phoumenavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,
 RA Stapleton M., Strong R., Svirskas R., Tector C., Tyler D.,
 RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
 RA "Sequencing of Drosophila melanogaster genome.";
 RA Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RA [3]
 RA SEQUENCE FROM N.A.
 RA Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
 RA Hradecky P., Huang Y., Kaminker J.S., Prochnik S.E., Smith C.D.,
 RA Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E.,
 RA Clamp M., Dysdale R., Emmert D., Frise E., de Grey A., Harris N.,
 RA Krommiller B., Marshall B., Milburn G., Richter J., Russo S.,
 RA Seearie S.M.J., Smith E., Shu S., Smutnick F., Whitfield E.,
 RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;
 RA "Annotation of Drosophila melanogaster genome.";
 RA Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RA [4]
 RA SEQUENCE FROM N.A.
 RA Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter J.C.;
 RA Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 RA [5]
 RA SEQUENCE FROM N.A.

RA FlyBase;
 RA Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AE003484; AAN09267.1;
 SO SEQUENCE 312 AA; 34214 MW; 78D5834E74E168DF CRC64;
 Query Match 81.0%; Score 1253.5; DB 5; Length 312;
 Best Local Similarity 81.2%; Pred. No. 8.1e-103;
 Matches 237; Conservative 21; Mismatches 33; Indels 1; Gaps 1;
 QY 5 ALSFADFLAGVAAAIKSTAVAPIERVKLLLOVHASKOITFADKOYKIDCVVRIPKE 64
 DB 20 AVGFVADFAAGGISAASVSKTAVAPIERVKLLLOVHASKOISPDOKYKAWDFIRIPKE 79
 QY 65 QEVLSFWRGNLANVIRFPTQALNFAFKDKYKQIFLGGVDKRTQYFWRYFAGNLASGAG 124
 DB 80 QGSFSEWRGNLANVIRFPTQALNFAFKDKYKQYFLLGGVDKNTQYFWRYFAGNLASGAG 139
 QY 125 ATSLCFYPPIDFATRIAAAVGAGAAERERGLDCLVKIKYKDGITKGLVQGVNSVQGI 184
 DB 140 ATSLCFYPPIDFATRIAAADTGK-GGQREFTGLNCLTKFKSDGIVGLRGFVSQGI 198
 QY 185 IIRAAVFGIYDTAKGLPDPKNTHTYISWMIQVTAVALGTSYFDPYRRRMMQSGR 244
 DB 199 IIRAAVFGIYDTAKGLPDPKNTHTYISWMIQVTAVALGTSYFDPYRRRMMQSGR 258
 QY 245 KGFDMYTGTLDCWRKIARDEGKAPFKGAMSVNLKMGAFVLYIDEIK 296
 DB 259 KATEVYIKNTLHCWATIAKEGTGAFKFAFNSILKGTGAFVLYIDEIK 310
 RESULT 13
 ID Q9NHWS PRELIMINARY; PRT; 300 AA.
 AC Q9NHWS;
 DT 01-OCT-2000 (TREMBLrel. 15, Created)
 DT 01-OCT-2000 (TREMBLrel. 15, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE ADP/ATP translocase.
 OS Lucilia cuprina (Greenbottle fly) (Australian sheep blowfly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestridae;
 OC Calliphoridae; Lucilla.
 OC NCBI_TaxID=7375;
 RN RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SS mal seeking;
 RA Chen Z., Fair J.A., Batterham P.;
 RT "A cDNA clone encoding the ADP/ATP translocase of Lucilla cuprina.";
 RU Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
 DR EMBL: AF218587; AAF32322.1; -;
 DR InterPro: IPR001993; Mitoch_carrier.
 DR InterPro: IPR002067; Mit_carrier.
 DR Pfam: PF00153; mito_carrt_3.
 DR PRINTS: PR00926; MITOCARRIER.
 DR PROSITE: PS00215; MITOCH_CARRIER; 3.
 KW Membrane; Transmembrane; Transport.
 SQ SEQUENCE 300 AA; 33036 MW; 5459DF0EA0E2E742 CRC64;
 Query Match 80.7%; Score 1248.5; DB 5; Length 300;
 Best Local Similarity 81.2%; Pred. No. 2.1e-102;
 Matches 237; Conservative 20; Mismatches 34; Indels 1; Gaps 1;
 QY 6 LSFAKFLAGVAAAIKSTAVAPIERVKLLLOVHASKOITADKOYKIDCVVRIPKEQ 65
 DB 9 LGFVKFPAAGGISAASVSKTAVAPIERVKLLLOVHASKOISPDOKYKGMIDCVVRIPKEQ 68
 QY 66 EVLSFWRGNLANVIRFPTQALNFAFKDKYKQIFLGGVDKRTQYFWRYFAGNLASGAG 125
 DB 69 GFASVWRGNLANVIRFPTQALNFAFKDKYKQYFLLGGVDKNTQYFWRYFAGNLASGAG 128
 QY 126 TSLCFYPPIDFATRIAAAVGAGAAERERGLDCLVKIKYKDGITKGLVQGVNSVQGI 185

DB 129 TSLCFVYPLDPAKRLAADTGK-GGQREFTGLGNCILAKIFKSDGLVGLYRGFVSVGGII 187
 QY 186 IYRAAYFGIYDTAKMLDPKRNTHIVISMIAQVTAVAGLSYSPFDVRRMMQSGRK 245
 DB 188 IYRAAYFEFYDPAKMLDPKRNTHIVISMIAQVTAVAGLSYSPFDVRRMMQSGRK 247
 QY 246 GTDLMYTGTLDCWKRIARDEGKAFFKGAWSNVLGNGAFVLYLDEIKKY 297
 DB 248 ATEIIYKNTLHCWATIAKQEGTGAFFKGAWSNVLGNGAFVLYLDEIKKF 299

RESULT 14

044093 PRELIMINARY: PRT: 288 AA.
 ID 044093
 AC 044093;
 DT 01-JUN-1998 (TREMBLrel. 06, Created)
 DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
 DE ADP/ATP translocase (Fragment).
 GN SESB.
 OS Drosophila pseudoobscura (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OC NCBI_TaxID=7237;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Zeng L.-W., Comeron J.M., Chen B., Kreitman M.;
 RL Genetics 0:0-0(1997).
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
 DR EMBL: AF025799; AAB87884.1; -.
 DR FLYbase: FBgn0023292; Dpse\sesb.
 DR InterPro: IPR001993; Mitoch_carrier.
 DR InterPro: IPR002067; Mit_carrier.
 DR Pfam: PF00153; mito_carr. 3.
 DR PRINTS: PR00926; MITOCARRIER.
 DR PROSITE: PS00215; MITOCH_CARRIER; 3.
 DR Membrane; Repeat; Transmembrane; Transport.
 KW NON_TER 288
 FT SEQUENCE 288 AA; 31725 MW; 052B0CC0050436B0 CRC64;

Query Match 77.0%; Score 1190.5; DB 5; Length 288;
 Best Local Similarity 80.4%; Pred. No. 2.8e-97;
 Matches 229; Conservative 20; Mismatches 33; Indels 3; Gaps 3;

QY 5 ALSFAKDLFAGVAAAIKSTAVAPIERVKLLQVOHASQIOTADKOYKGIIDCVRIPE 64
 DB 7 AIGFVYDFDPAKMLDPKRNTHIVISMIAQVTAVAGLSYSPFDVRRMMQSGRK 66
 QY 65 QEVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGVDKRTQFWRYPAGNLAGSGAAG 124
 DB 67 QGFSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGVDKRTQFWRYPAGNLAGSGAAG 126
 QY 125 ATSLCFVYPLDPAKRLAADVGKAGAREFRGLGDCLVKITYSDGIGKLYGCFNVSVOGI 184
 DB 127 ATSLCFVYPLDPAKRLAADVGKAGAREFRGLGDCLVKITYSDGIGKLYGCFNVSVOGI 185
 QY 185 IYRAAYFGIYDTAKMLDPKRNTHIVISMIAQVTAVAGLSYSPFDVRRMMQSGRK 244
 DB 186 IYRAAYFEFYDPAKMLDPKRNTHIVISMIAQVTAVAGLSYSPFDVRRMMQSGRK 244
 QY 245 KGTDIYTGTLDCWKRIARDEGKAFFKGAWSNVLGNGAFVLYL 289
 DB 245 KATEIIYKNTLHCWATIAKQEGTGAFFKGAWSNVLGNGAFVLY 288

RESULT 15

044094 PRELIMINARY: PRT: 288 AA.
 ID 044094;
 AC 044094;
 DT 01-JUN-1998 (TREMBLrel. 06, Created)
 DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
 DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)

DE ADP/ATP translocase (Fragment).
 GN SESB.
 OS Drosophila subobscura (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 OC NCBI_TaxID=7241;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Zeng L.-W., Comeron J.M., Chen B., Kreitman M.;
 RL Genetics 0:0-0(1997).
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
 DR EMBL: AF025799; AAB87884.1; -.
 DR FLYbase: FBgn0023292; Dpse\sesb.
 DR InterPro: IPR001993; Mitoch_carrier.
 DR InterPro: IPR002067; Mit_carrier.
 DR Pfam: PF00153; mito_carr. 3.
 DR PRINTS: PR00926; MITOCARRIER.
 DR PROSITE: PS00215; MITOCH_CARRIER; 3.
 DR Membrane; Repeat; Transmembrane; Transport.
 KW NON_TER 288
 FT SEQUENCE 288 AA; 31775 MW; 06A1D1E477E81B26 CRC64;

Query Match 76.6%; Score 1185.5; DB 5; Length 288;
 Best Local Similarity 80.0%; Pred. No. 7.7e-97;
 Matches 228; Conservative 21; Mismatches 33; Indels 3; Gaps 3;

QY 5 ALSFAKDLFAGVAAAIKSTAVAPIERVKLLQVOHASQIOTADKOYKGIIDCVRIPE 64
 DB 7 AMGFVYDFDPAKMLDPKRNTHIVISMIAQVTAVAGLSYSPFDVRRMMQSGRK 66
 QY 65 QEVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGVDKRTQFWRYPAGNLAGSGAAG 124
 DB 67 QGFSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGVDKRTQFWRYPAGNLAGSGAAG 126
 QY 125 ATSLCFVYPLDPAKRLAADVGKAGAREFRGLGDCLVKITYSDGIGKLYGCFNVSVOGI 184
 DB 127 ATSLCFVYPLDPAKRLAADVGKAGAREFRGLGDCLVKITYSDGIGKLYGCFNVSVOGI 185
 QY 185 IYRAAYFGIYDTAKMLDPKRNTHIVISMIAQVTAVAGLSYSPFDVRRMMQSGRK 244
 DB 186 IYRAAYFEFYDPAKMLDPKRNTHIVISMIAQVTAVAGLSYSPFDVRRMMQSGRK 244
 QY 245 KGTDIYTGTLDCWKRIARDEGKAFFKGAWSNVLGNGAFVLY 289
 DB 245 KATEIIYKNTLHCWATIAKQEGTGAFFKGAWSNVLGNGAFVLY 288

Search completed: August 28, 2003, 19:42:10
 Job time : 51.3897 secs

PA (MITO-) MITOKOR.
 XX
 PI Anderson CM, Davis RE, Clevenger W, Wiley SE, Miller SW, Szabo TR;
 PI Ghosh SS;
 XX
 DR WPI: 2000-365619/31.
 DR N-PSDB: AAD00521.
 XX
 PT Recombinant construct encoding adenine nucleotide translocator
 PT polypeptide, useful e.g. in screening for potential therapeutic agents
 PT against mitochondrial disease -
 XX
 PS Claim 46; Page 173-174; 175pp; English.
 XX
 CC The patent discloses a method to produce adenine nucleotide translocator
 CC (ANT) proteins or ANT fusion proteins using recombinant expression
 CC constructs. ANT is a nuclear encoded protein and a major component of
 CC inner mitochondrial membrane. It mediates transport of adenosine
 CC d/tri-phosphates across the mitochondrial inner membrane and also serves
 CC as an important molecular component of the mitochondrial permeability
 CC transition pore, a modulator of apoptosis. ANT is used to identify agents
 CC or ligands that bind to, or interact with it. The ANT ligands are used to
 CC detect or isolate ANT in a biological sample, and therapeutically for
 CC regulating mitochondrial pore activity for treating diseases associated
 CC with altered mitochondrial function, including Alzheimer's, Parkinson's
 CC and Huntington's diseases, cancer, psoriasis, diabetes, dystonia,
 CC Leber's hereditary optic neuropathy, schizophrenia, mitochondrial
 CC encephalopathy, lactic acidosis and stroke (MELAS), hyperproliferative
 CC disorders, mitochondrial diabetes and deafness (MIDN), and myoclonic
 CC epilepsy red ragged fibre syndrome. The present sequence is an
 CC adenine nucleotide translocator ANT3 from human brain.
 CC
 XX
 SQ Sequence 298 AA;
 Query Match 100.0%; Score 1543; DB 21; Length 298;
 Best Local Similarity 100.0%; Pred. No. 4, 6e-157;
 Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MTEQATSPAKDFLAGGIAAIAISKTAAVPIERVKLLQOVHASKQIADKQYKIVDCIYR 60
 DB 1 MTEQATSPAKDFLAGGIAAIAISKTAAVPIERVKLLQOVHASKQIADKQYKIVDCIYR 60
 QY 61 IPEQGVLSFWKGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFWRYPAGNLAGS 120
 DB 61 IPEQGVLSFWKGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFWRYPAGNLAGS 120
 QY 121 GAAGATSLCFVYPLDPAFRTRLADVGKSGTEREFGDGLVYITKSDGIRGLYQGFVS 180
 DB 121 GAAGATSLCFVYPLDPAFRTRLADVGKSGTEREFGDGLVYITKSDGIRGLYQGFVS 180
 QY 122 GAAGATSLCFVYPLDPAFRTRLADVGKSGTEREFGDGLVYITKSDGIRGLYQGFVS 180
 DB 122 GAAGATSLCFVYPLDPAFRTRLADVGKSGTEREFGDGLVYITKSDGIRGLYQGFVS 180
 QY 181 VGGIITIRAAVFGVYDTAKGMLPDPKNTHTIVSWMTAQTVTAAGVSYPTDTRRRMM 240
 DB 181 VGGIITIRAAVFGVYDTAKGMLPDPKNTHTIVSWMTAQTVTAAGVSYPTDTRRRMM 240
 QY 241 QSGRGADIMYTGTCWKRIFDEGKAFKFGKANSNVLRGKAGAVLYLYDELKRYI 298
 DB 241 QSGRGADIMYTGTCWKRIFDEGKAFKFGKANSNVLRGKAGAVLYLYDELKRYI 298
 DB 241 QSGRGADIMYTGTCWKRIFDEGKAFKFGKANSNVLRGKAGAVLYLYDELKRYI 298

KM chemokine; thrombolytic; drug screening; arthritis; inflammation;
 KM leukaemia.
 XX
 OS Homo sapiens.
 XX
 PN WO200153312-A1.
 XX
 PD 26-JUL-2001.
 XX
 PF 26-DEC-2000; 2000WO-US34263.
 XX
 PR 21-JAN-2000; 2000US-0488725.
 PR 25-APR-2000; 2000US-0552317.
 PR 09-JUL-2000; 2000US-0598042.
 PR 19-JUL-2000; 2000US-0620312.
 PR 03-AUG-2000; 2000US-0653450.
 PR 14-SEP-2000; 2000US-0662191.
 PR 19-OCT-2000; 2000US-0693036.
 PR 29-NOV-2000; 2000US-0727344.
 XX
 PA (HYSE-) HYSEQ INC.
 XX
 PI Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
 PI Wang J, Wang Z, Wehrman T, Xu C, Xue AJ, Yang Y, Zhang J;
 PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;
 XX
 DR WPI: 2001-442253/47.
 DR N-PSDB: AAI58797.
 XX
 PT Novel nucleic acids and polypeptides, useful for treating disorders
 PT such as central nervous system injuries -
 XX
 PS Example 4; SEQ ID NO 2786; 10078pp; English.
 XX
 CC The invention relates to human nucleic acids (AAI57798-AAI61369) and
 CC the encoded polypeptides (AAI38642-AAI42213) with neurotrophic,
 CC immunosuppressant and cytostatic activity. The polynucleotides are useful
 CC in gene therapy. A composition containing a polypeptide or polynucleotide
 CC of the invention may be used to treat diseases of the peripheral nervous
 CC system, such as peripheral nervous injuries, peripheral neuropathy and
 CC localized neuropathies and central nervous system diseases, such as
 CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
 CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
 CC utilisation of the activities such as: Immune system suppression,
 CC Actin/Inhibin activity, chemocytic/chemokine activity, haemostatic
 CC and thrombolytic activity, cancer diagnosis and therapy, drug screening
 CC assays for receptor activity, arthritis and inflammation, leukaemia and
 CC C.N.S disorders.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification.
 CC
 XX
 SQ Sequence 298 AA;
 Query Match 100.0%; Score 1543; DB 22; Length 298;
 Best Local Similarity 100.0%; Pred. No. 4, 6e-157;
 Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MTEQATSPAKDFLAGGIAAIAISKTAAVPIERVKLLQOVHASKQIADKQYKIVDCIYR 60
 DB 1 MTEQATSPAKDFLAGGIAAIAISKTAAVPIERVKLLQOVHASKQIADKQYKIVDCIYR 60
 QY 61 IPEQGVLSFWKGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFWRYPAGNLAGS 120
 DB 61 IPEQGVLSFWKGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFWRYPAGNLAGS 120
 QY 121 GAAGATSLCFVYPLDPAFRTRLADVGKSGTEREFGDGLVYITKSDGIRGLYQGFVS 180
 DB 121 GAAGATSLCFVYPLDPAFRTRLADVGKSGTEREFGDGLVYITKSDGIRGLYQGFVS 180
 QY 122 GAAGATSLCFVYPLDPAFRTRLADVGKSGTEREFGDGLVYITKSDGIRGLYQGFVS 180
 DB 122 GAAGATSLCFVYPLDPAFRTRLADVGKSGTEREFGDGLVYITKSDGIRGLYQGFVS 180
 QY 181 VGGIITIRAAVFGVYDTAKGMLPDPKNTHTIVSWMTAQTVTAAGVSYPTDTRRRMM 240
 DB 181 VGGIITIRAAVFGVYDTAKGMLPDPKNTHTIVSWMTAQTVTAAGVSYPTDTRRRMM 240
 DB 181 VGGIITIRAAVFGVYDTAKGMLPDPKNTHTIVSWMTAQTVTAAGVSYPTDTRRRMM 240

```

OY 241 QSGRGADIMTGTVDCKRKIFRDEGKAFKFGAMSNVLRGNGAFVLYLDELKVI 298
DB 241 QSGRGADIMTGTVDCKRKIFRDEGKAFKFGAMSNVLRGNGAFVLYLDELKVI 298

RESULT 3
AAU01200
ID AAU01200 standard; Protein; 298 AA.
XX
AC AAU01200;
XX
DE 07-SEP-2001 (first entry)
XX
DE Human adenine nucleotide translocator-3 (ANT-3) protein.
XX
KW Human; adenine nucleotide translocator-3; ANT-3; MTP; cyclophilin;
KW mitochondrial permeability transition pore component; cell survival;
KW mitochondrial core component; mitochondrial related disorder; cancer;
KW Alzheimer's disease; diabetes mellitus; hyperproliferative disorder.
XX
OS Homo sapiens.
XX
PN MO200132876-A2.
XX
PD 10-MAY-2001.
XX
PF 03-NOV-2000; 2000WO-US30535.
XX
PR 03-NOV-1999; 99US-0434354.
XX
PA (MITO-) MITOKOR.
XX
PI Murphy AN, Clevenger W, Wiley SE, Andreyev AY, Frigeri IG;
PI Vellicelebi G, Davis RE;
PI MPI: 2001-291054/30.
XX
DR N-PSDB; AAS05903.
XX
PT New nucleic acid expression constructs, useful for screening for agents
PT that alter mitochondrial permeability transition (MPT), comprises
PT polynucleotide encoding MPT polypeptide or cyclophilin polypeptide
PT fused to energy transfer molecule -
XX
PS Disclosure; Fig 2; 186pp; English.
XX
CC The present sequence represents human adenine nucleotide translocator-3
CC (ANT-3) protein. ANT proteins are mitochondrial permeability
CC transition (MPT) pore components responsible for mediating transport
CC of ADP across the mitochondrial inner membrane. ANT proteins interact
CC with other mitochondrial core components e.g. cyclophilins to
CC regulate MPT. The present invention relates to a novel nucleic acid
CC expression construct comprising a promoter operably linked to a
CC polynucleotide encoding a mitochondrial pore component polypeptide
CC (e.g. ANT) fused to an energy transfer molecule (ETM) protein
CC (e.g. green fluorescent protein (GFP) or a FLASH sequence). The novel
CC expression construct can alter mitochondrial membrane permeability
CC transition and/or alter the interaction between mitochondrial core
CC components. The methods are useful for screening for agents that alter
CC MPT and/or cell survival. These agents are useful for the prevention or
CC treatment of diseases associated with altered mitochondrial function or
CC dysfunctional cell survival, such as Alzheimer's disease, diabetes
CC mellitus, Parkinson's disease, Huntington's disease, schizophrenia,
CC mitochondrial encephalopathy, lactic acidosis, stroke,
CC hyperproliferative disorders e.g. cancer, and deafness.
XX
SQ Sequence 298 AA;

Query Match 100.0%; Score 1543; DB 22; Length 298;
Best Local Similarity 100.0%; Pred. No. 4,66-157;
Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
OY 1 MTEQAISFAKDFLAGIAAIAISKTAVAPIERVKLLLOVQHASKQIAADKQYGIYDCIYR 60
|||||

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DB 1 MTEQAISFAKDFLAGIAAIAISKTAVAPIERVKLLLOVQHASKQIAADKQYGIYDCIYR 60
OY 61 IPKEGVLSFWMGNLANVIRYPTQALNFAFDKXKQJFLGVDKHTQFWRFYAGNLASG 120
DB 61 IPKEGVLSFWMGNLANVIRYPTQALNFAFDKXKQJFLGVDKHTQFWRFYAGNLASG 120
OY 121 GAAGATSLCEVYPLDFARTRLADYVKGSGTEERFRLGDCLVKIRKSDGIRGLYOGFSYS 180
DB 121 GAAGATSLCEVYPLDFARTRLADYVKGSGTEERFRLGDCLVKIRKSDGIRGLYOGFSYS 180
OY 181 VOGIIIRYRAAYGVYDTAKGMLPDPKNTIHIVSMIAQVTVAAGVSYPTPTVRRMM 240
DB 181 VOGIIIRYRAAYGVYDTAKGMLPDPKNTIHIVSMIAQVTVAAGVSYPTPTVRRMM 240
OY 241 QSGRGADIMTGTVDCKRKIFRDEGKAFKFGAMSNVLRGNGAFVLYLDELKVI 298
DB 241 QSGRGADIMTGTVDCKRKIFRDEGKAFKFGAMSNVLRGNGAFVLYLDELKVI 298

RESULT 4
AAU10380
ID AAU10380 standard; Protein; 298 AA.
XX
AC AAU10380;
XX
DE 14-FEB-2002 (first entry)
XX
DE Human adenine nucleotide translocator 3 (ANT3).
XX
KW Human; adenine nucleotide translocator; ANT;
KW mitochondrial matrix protein.
XX
OS Homo sapiens.
XX
PN WO200185944-A2.
XX
PD 15-NOV-2001.
XX
PF 11-MAY-2001; 2001WO-US15416.
XX
PR 11-MAY-2000; 2000US-0569327.
XX
PA (MITO-) MITOKOR.
XX
PI Anderson CM, Davis RE, Clevenger W, Wiley SE, Miller SM, Szabo TR;
PI Ghosh SS, Moos WT, Pel Y, Carroll AK;
PI MPI: 2002-055598/07.
XX
DR N-PSDB; AAS16690.
XX
PT Novel recombinant expression construct for producing adenine nucleotide
PT translocator polypeptides, comprises a regulated promoter linked to
PT nucleic acid encoding the polypeptide -
XX
PS Example 3; Fig 2; 147pp; English.
XX
CC The invention relates to a recombinant expression construct (I)
CC comprising a regulated promoter operably linked to a nucleic acid
CC encoding an adenine nucleotide translocator (ANT) polypeptide. ANT
CC proteins mediate the exchange of ATP synthesized in the mitochondrial
CC matrix for ADP in the cytosol. (I) is useful for producing recombinant
CC ANT polypeptide by transforming a prokaryotic or eukaryotic host cell and
CC culturing the host cell. (I) is also useful for targeting a polypeptide
CC of interest to a mitochondrial membrane, where ANT polypeptide is
CC expressed as a fusion protein with the polypeptide of interest.
CC Recombinant ANT polypeptide, or cells expressing the polypeptide, is
CC useful for identifying an agent that binds to an ANT polypeptide. ANT
CC ligand is useful for determining the presence of an ANT polypeptide;
CC preferably ANT1, ANT2 or ANT3 in a biological sample and for isolating
CC ANT from a biological sample, where the ANT ligand is covalently or non-
CC covalently bound to a solid phase. Detectably labeled ANT ligand is also
CC useful for identifying an agent that interacts with an ANT polypeptide.
CC The present sequence represents the amino acid sequence of human ANT3.

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XX Sequence 298 AA;
Query Match 100.0%; Score 1543; DB 23; Length 298;
Best Local Similarity 100.0%; Pred. No. 4, 6e-157;
Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MTEQAIISFANDFLAGGIAAISKTAAPRIERVKLLQVQHASQIOADKQYKGIQDICTR 60
DB 1 MTEQAIISFANDFLAGGIAAISKTAAPRIERVKLLQVQHASQIOADKQYKGIQDICTR 60
QY 61 IPKEQGLSFWKRGNLAVIRYFPQALNFAFKDKYKQIFLGVDKHTQFRRYFAGNLSG 120
DB 61 IPKEQGLSFWKRGNLAVIRYFPQALNFAFKDKYKQIFLGVDKHTQFRRYFAGNLSG 120
QY 121 GAAGATSLCFVYPLDFARTRLADVGSCTEREPRGIGDCLVITKSDGIRGLYQGSVS 180
DB 121 GAAGATSLCFVYPLDFARTRLADVGSCTEREPRGIGDCLVITKSDGIRGLYQGSVS 180
QY 181 VGGIIIRAAVFGVYDTAKGMLPDPKNTHTIVSMIAQVTAAGVVSYPEDTVRRMM 240
DB 181 VGGIIIRAAVFGVYDTAKGMLPDPKNTHTIVSMIAQVTAAGVVSYPEDTVRRMM 240
QY 241 QSGRKADIMYTGTVDCWKRIKIFRDEGKAFKGAWSNVLKMGAFVLVLYDELKVI 298
DB 241 QSGRKADIMYTGTVDCWKRIKIFRDEGKAFKGAWSNVLKMGAFVLVLYDELKVI 298
RESULT 5
ID AAM41427 standard; Protein: 323 AA.
AC AAM41427;
XX 22-OCT-2001 (first entry)
DT Human polypeptide SEQ ID NO 6358.
DE Human polypeptide SEQ ID NO 6358.
XX Human; noctropic; immunosuppressant; cytostatic; gene therapy; cancer;
KW peripheral nervous system; neuropathy; central nervous system; CNS;
KW Alzheimer's; Parkinson's disease; Huntington's disease; haemostatic;
KW amyotrophic lateral sclerosis; Shy-Drager Syndrome; chemotactic;
KW chemokine; thrombolytic; drug screening; arthritis; inflammation;
KW Leukaemia.
XX Homo sapiens.
OS
XX MO200153312-A1.
PN
XX 26-JUL-2001.
PD
XX 26-DEC-2000; 2000MO-US34263.
PF
XX 21-JAN-2000; 2000US-0488725.
PR 25-APR-2000; 2000US-0552317.
PR 09-JUL-2000; 2000US-0598042.
PR 19-JUL-2000; 2000US-0620312.
PR 03-AUG-2000; 2000US-0653450.
PR 14-SEP-2000; 2000US-0662191.
PR 19-OCT-2000; 2000US-0693036.
PR 29-NOV-2000; 2000US-0727344.
XX
XX (HYSE-) HYSEQ INC.
XX
XX Tang YT, Liu C, Asundi V, Chen R, Ma Y, Qian XB, Ren F, Wang D;
PI Wang J, Wang Z, Wehman T, Xu C, Xue AJ, Yang Y, Zhang J;
PI Zhao QA, Zhou P, Goodrich R, Drmanac RT;
XX
XX WPI; 2001-442253/47.
DR N-PDB; AAI60583.
XX
XX Novel nucleic acids and polypeptides, useful for treating disorders
PT such as central nervous system injuries -

XX Example 2: SEQ ID NO 6358; 10078pp; English.
PS
XX The invention relates to human nucleic acids (AA157798-AA161369) and
CC the encoded polypeptides (AAM38642-AAM42213) with noctropic,
CC immunosuppressant and cytostatic activity. The polynucleotides are useful
CC in gene therapy. A composition containing a polypeptide or polynucleotide
CC of the invention may be used to treat diseases of the peripheral nervous
CC system, such as peripheral nervous injuries, peripheral neuropathy and
CC localised neuropathies and central nervous system diseases, such as
CC Alzheimer's, Parkinson's disease, Huntington's disease, amyotrophic
CC lateral sclerosis, and Shy-Drager Syndrome. Other uses include the
CC utilisation of the activities such as: Immune system suppression,
CC Activin/Inhibin activity, chemotactic/chemokine activity, haemostatic
CC and thrombolytic activity, cancer diagnosis and therapy, drug screening,
CC assays for receptor activity, arthritis and inflammation, leukaemias and
CC C.N.S disorders.
CC Note: The sequence data for this patent did not form part of the printed
CC specification.
XX
XX Sequence 323 AA;
Query Match 100.0%; Score 1543; DB 22; Length 323;
Best Local Similarity 100.0%; Pred. No. 5, 2e-157;
Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MTEQAIISFANDFLAGGIAAISKTAAPRIERVKLLQVQHASQIOADKQYKGIQDICTR 60
DB 26 MTEQAIISFANDFLAGGIAAISKTAAPRIERVKLLQVQHASQIOADKQYKGIQDICTR 85
QY 61 IPKEQGLSFWKRGNLAVIRYFPQALNFAFKDKYKQIFLGVDKHTQFRRYFAGNLSG 120
DB 61 IPKEQGLSFWKRGNLAVIRYFPQALNFAFKDKYKQIFLGVDKHTQFRRYFAGNLSG 120
QY 86 IPKEQGLSFWKRGNLAVIRYFPQALNFAFKDKYKQIFLGVDKHTQFRRYFAGNLSG 145
DB 86 IPKEQGLSFWKRGNLAVIRYFPQALNFAFKDKYKQIFLGVDKHTQFRRYFAGNLSG 145
QY 121 GAAGATSLCFVYPLDFARTRLADVGSCTEREPRGIGDCLVITKSDGIRGLYQGSVS 180
DB 146 GAAGATSLCFVYPLDFARTRLADVGSCTEREPRGIGDCLVITKSDGIRGLYQGSVS 205
QY 181 VGGIIIRAAVFGVYDTAKGMLPDPKNTHTIVSMIAQVTAAGVVSYPEDTVRRMM 240
DB 206 VGGIIIRAAVFGVYDTAKGMLPDPKNTHTIVSMIAQVTAAGVVSYPEDTVRRMM 265
QY 241 QSGRKADIMYTGTVDCWKRIKIFRDEGKAFKGAWSNVLKMGAFVLVLYDELKVI 298
DB 266 QSGRKADIMYTGTVDCWKRIKIFRDEGKAFKGAWSNVLKMGAFVLVLYDELKVI 323
RESULT 6
ID AAO18516 standard; Protein: 298 AA.
AC AAO18516;
XX 11-OCT-2002 (first entry)
DT Human insulin receptor signaling modifier SEQ ID NO: 54.
DE Human insulin receptor signaling modifier; insulin receptor signaling modifier;
KW Human; insulin receptor signaling; insulin receptor signaling modifier;
KW IEM; diabetes; metabolic syndrome; antidiabetic.
XX
XX Homo sapiens.
OS
XX MO200255664-A2.
PN
XX 18-JUL-2002.
PD
XX 11-JAN-2002; 2002MO-US01048.
PF
XX 12-JAN-2001; 2001US-261226P.
PR 12-JAN-2001; 2001US-261303P.
PR 12-JAN-2001; 2001US-261304P.
PR 12-JAN-2001; 2001US-261335P.
PR 12-JAN-2001; 2001US-261336P.

PR 12-JAN-2001; 2001US-261361P.
 PR 12-JAN-2001; 2001US-261456P.
 PR 12-JAN-2001; 2001US-261457P.
 PR 12-JAN-2001; 2001US-261458P.
 PR 12-JAN-2001; 2001US-261459P.
 PR 12-JAN-2001; 2001US-261461P.
 PR 12-JAN-2001; 2001US-261518P.
 PR 12-JAN-2001; 2001US-261531P.
 PR 12-JAN-2001; 2001US-261532P.
 PR 12-JAN-2001; 2001US-261589P.
 PR 12-JAN-2001; 2001US-261590P.
 PR 12-JAN-2001; 2001US-261694P.
 PR 12-JAN-2001; 2001US-261695P.
 PR 12-JAN-2001; 2001US-261697P.
 XX
 XX (EXEL-) EXELIXIS INC.
 XX
 PR Seidel-Dugan C, Ferguson KC, Kidd T;
 XX
 DR WPI: 2002-599664/64.
 DR N-PSDB; NAL48635.
 XX
 PT Identifying an insulin receptor signaling modulator, useful as drug
 PT targets for treating diabetes or metabolic disorders, comprises
 PT contacting an assay system comprising insulin receptor signaling
 PT modifiers with a test agent
 XX
 PS Disclosure: Page 160-161; 232pp; English.

CC The present invention relates to a method of identifying a candidate
 CC Insulin receptor (INR) signaling modulating agent, involving contacting
 CC an assay system comprising an insulin receptor signaling modifier (ISM)
 CC polypeptide or nucleic acid with a test agent, and detecting a test
 CC agent-biased activity of the assay system. The method is useful for
 CC identifying candidate INR signaling modulating agents. ISM genes may be
 CC used as drug targets for treatment of disorders related to INR signaling
 CC such as diabetes or metabolic syndrome. ISM nucleic acids and
 CC polypeptides are useful for identifying and testing agents that modulate
 CC ISM function and for other applications related to the involvement of ISM
 CC in INR signaling, and for identifying subjects having a predisposition to
 CC such diseases associated with INR signaling. The present sequence is an
 CC ISM protein described in the exemplification of the invention.

SQ Sequence 298 AA;

Query Match 94.8%; Score 1463; DB 23; Length 298;

Best Local Similarity 92.9%; Pred. No. 1.8e-148; Indels 0; Gaps 0;

Matches 275; Conservative 13; Mismatches 8; Indels 0; Gaps 0;

QY 1 MTEQAISPAKDFLAGIAAISTKTAAPRIERVKLLQVOHASKQIADKQYGIYDCIYR 60
 DB 1 MTDAAVSPAKDFLAGVAAIAISTKTAAPRIERVKLLQVOHASKQIADKQYGIYDCIYR 60
 QY 61 IPKEGVLSFWRGNTANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFWRFAQNLASG 120
 DB 61 IPKEGVLSFWRGNTANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFWRFAQNLASG 120
 QY 121 GAAGATSCFVYPLDFARTRLAADYKSGTEREFGDCLVTKIKSGIRGLYGFSSVS 180
 DB 121 GAAGATSCFVYPLDFARTRLAADYKSGTEREFGDCLVTKIKSGIRGLYGFSSVS 180
 QY 181 VOGIITVRAAFGVYDTAKGMLPDKNTHIVVSMIAOTVTVAGVSVYPTVRRMM 240
 DB 181 VOGIITVRAAFGVYDTAKGMLPDKNTHIVVSMIAOTVTVAGVSVYPTVRRMM 240
 QY 241 QSGRKADIMYTGIVDCNRKRFIRDEGKAFFKGAANSNVLKMGAFVLVLYDELK 296
 DB 241 QSGRKADIMYTGIVDCNRKRFIRDEGKAFFKGAANSNVLKMGAFVLVLYDELK 296
 QY 241 QSGRKADIMYTGIVDCNRKRFIRDEGKAFFKGAANSNVLKMGAFVLVLYDELK 296
 DB 241 QSGRKADIMYTGIVDCNRKRFIRDEGKAFFKGAANSNVLKMGAFVLVLYDELK 296

RESULT 7
 AAY71032
 ID AAY71032 standard; Protein; 298 AA.

XX
 AC AAY71032;
 XX
 DT 29-AUG-2000 (first entry)
 XX
 DE Human adenine nucleotide translocator ANT2.
 XX

Human; adenine nucleotide translocator; ANT2; mitochondria; ADP; ATP;
 KW adenosine di-phosphate; adenosine tri-phosphate; apoptosis; MPT; cancer;
 KW mitochondrial permeability transition; neuroprotective; nontoxic;
 KW antiParkinsonian; cytosolic; antidiabetic; anticonvulsant; neuroleptic;
 KW antiparkinson; cerebroprotective; therapeutic; screening; psoriasis;
 KW Alzheimer's disease; Parkinson's disease; Huntington's disease; dystonia;
 KW diabetes; Leber's hereditary optic neuropathy; schizophrenia; MELAS;
 KW mitochondrial encephalopathy; lactic acidosis; stroke; MIDP;
 KW mitochondrial diabetes and deafness; hyperproliferative disorder;
 KW myoclonic epilepsy red ragged fibre syndrome.

XX Homo sapiens.
 XX
 PN WO200026370-A2.
 XX
 XX 11-MAY-2000.
 XX

XX 03-NOV-1999; 99WO-US25883.
 XX
 XX 03-NOV-1998; 98US-0185904.
 XX 08-SEP-1999; 99US-0393441.
 XX

XX (MITO-) MITOKOR.

XX Anderson CM, Davis RE, Clevenger W, Wiley SE, Miller SW, Szabo TR;
 XX Ghosh SS;
 DR WPI: 2000-365619/31.
 DR N-PSDB; AAD00520.
 XX

PT Recombinant construct encoding adenine nucleotide translocator
 PT polypeptide, useful e.g. in screening for potential therapeutic agents
 PT against mitochondrial disease
 XX
 PS Claim 45; Page 172-173; 175pp; English.

CC The patent discloses a method to produce adenine nucleotide translocator
 CC (ANT) proteins or ANT fusion proteins using recombinant expression
 CC constructs. ANT is a nuclear encoded protein and a major component of
 CC inner mitochondrial membrane. It mediates transport of adenosine
 CC di/tri-phosphates across the mitochondrial inner membrane and also serves
 CC as an important molecular component of the mitochondrial permeability
 CC transition pore, a modulator of apoptosis. ANT is used to identify agents
 CC or ligands that bind to, or interact with it. The ANT ligands are used to
 CC detect or isolate ANT in a biological sample, and therapeutically for
 CC regulating mitochondrial pore activity, for treating diseases associated
 CC with altered mitochondrial function, including Alzheimer's, Parkinson's
 CC and Huntington's diseases, cancer, psoriasis, diabetes, dystonia,
 CC Leber's hereditary optic neuropathy, schizophrenia, mitochondrial
 CC encephalopathy, lactic acidosis and stroke (MELAS), hyperproliferative
 CC disorders, mitochondrial diabetes and deafness (MIDP), and myoclonic
 CC epilepsy red ragged fibre syndrome. The present sequence is an
 CC adenine nucleotide translocator ANT2 from human brain.

SQ Sequence 298 AA;

Query Match 94.2%; Score 1454; DB 21; Length 298;

Best Local Similarity 92.6%; Pred. No. 1.7e-147; Indels 0; Gaps 0;

Matches 274; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

QY 1 MTEQAISPAKDFLAGIAAISTKTAAPRIERVKLLQVOHASKQIADKQYGIYDCIYR 60
 DB 1 MTDAAVSPAKDFLAGVAAIAISTKTAAPRIERVKLLQVOHASKQIADKQYGIYDCIYR 60
 QY 61 IPKEGVLSFWRGNTANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFWRFAQNLASG 120
 DB 61 IPKEGVLSFWRGNTANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFWRFAQNLASG 120

Db 61 IPKEQEVLSFWRGNLANVIRYFPQALNFAFKDKYKQIFLGVDKRTQFRRYFAGNLASG 120
 QY 121 GAAGATSLCFVYPLDFARTRLADVKGSGTEREFGDGLVYTKSDGIRGLYQGFNS 180
 Db 121 GAAGATSLCFVYPLDFARTRLADVKGAGEREFRGLDGLVYTKSDGIRGLYQGFNS 180
 QY 181 VGGIIIRAAVFGVYDTAKGMLDPKNTHTIVSMIAQYTAAGVSYFEDVRRRRMM 240
 Db 181 VGGIIIRAAVFGVYDTAKGMLDPKNTHTIVSMIAQYTAAGVSYFEDVRRRRMM 240
 QY 241 QSGRKADIMYTGTVDCWKRIFRDEGGAFFKGAWSNVLRMGAFVLYLYDELK 296
 Db 241 QSGRKADIMYTGTVDCWKRIFRDEGGAFFKGAWSNVLRMGAFVLYLYDELK 296
 RESULT 8
 AAU01199
 ID AAU01199 standard; Protein; 298 AA.
 AC AAU01199;
 XX 07-SEP-2001 (first entry)
 DE Human adenine nucleotide translocator-2 (ANT-2) protein.
 XX
 KW Human; adenine nucleotide translocator-2; ANT-2; MTP; cyclophilin;
 KM mitochondrial permeability transition pore component; cell survival;
 KM mitochondrial core component; mitochondrial related disorder; cancer;
 KM Alzheimer's disease; diabetes mellitus; hyperproliferative disorder.
 XX
 OS Homo sapiens.
 XX
 PN WO200132876-A2.
 PD 10-MAY-2001.
 PF 03-NOV-2000; 2000WO-US03535.
 PR 03-NOV-1999; 9905-0434354.
 PA (MITO-) MITOKOR.
 PI Murphy AN, Cleverger W, Wiley SE, Andreyev AV, Frigeri LG;
 PI Velicelebi G, Davis RE;
 DR MPI; 2001-291054/30.
 XX N-PSDB; AAS05902.
 PT New nucleic acid expression constructs, useful for screening for agents
 PT that alter mitochondrial permeability transition (MPT), comprises
 PT polynucleotide encoding MPT polypeptide or cyclophilin polypeptide
 PT fused to energy transfer molecule -
 XX
 PS Disclosure; Fig 2; 186pp; English.
 CC The present sequence represents human adenine nucleotide translocator-2
 CC (ANT-2) protein. ANT proteins are mitochondrial permeability
 CC transition (MPT) pore components responsible for mediating transport
 CC of ADP across the mitochondrial inner membrane. ANT proteins interact
 CC with other mitochondrial core components e.g. cyclophilins to
 CC regulate MPT. The present invention relates to a novel nucleic acid
 CC expression construct comprising a promoter operably linked to a
 CC polynucleotide encoding a mitochondrial pore component polypeptide
 CC (e.g. ANT) fused to an energy transfer molecule (ETM) protein
 CC (e.g. green fluorescent protein (GFP) or a FLASH sequence). The novel
 CC expression construct can alter mitochondrial membrane permeability
 CC transition and/or alter the interaction between mitochondrial core
 CC components. The methods are useful for screening for agents that alter
 CC MPT and/or cell survival. These agents are useful for the prevention or
 CC treatment of diseases associated with altered mitochondrial function or
 CC dysfunctional cell survival, such as Alzheimer's disease, diabetes
 CC mellitus, Parkinson's disease, Huntington's disease, schizophrenia,
 CC mitochondrial encephalopathy, lactic acidosis, stroke,

CC hyperproliferative disorders e.g. cancer, and deafness.
 XX
 SQ Sequence 298 AA;
 Query Match 94.28; Score 1454; DB 22; Length 298;
 Best Local Similarity 92.68; Pred. No. 1.7e-147;
 Matches 274; Conservative 13; Mismatches 9; Indels 0; Gaps 0;
 QY 1 MTEQALISFANDFLAGINAISKTAVAPIRERKLLLOVQASHKQIADKQKGIYDCIVR 60
 Db 1 MTEQALISFANDFLAGINAISKTAVAPIRERKLLLOVQASHKQIADKQKGIYDCIVR 60
 QY 61 IPKEQEVLSFWRGNLANVIRYFPQALNFAFKDKYKQIFLGVDKRTQFRRYFAGNLASG 120
 Db 61 IPKEQEVLSFWRGNLANVIRYFPQALNFAFKDKYKQIFLGVDKRTQFRRYFAGNLASG 120
 QY 121 GAAGATSLCFVYPLDFARTRLADVKGSGTEREFGDGLVYTKSDGIRGLYQGFNS 180
 Db 121 GAAGATSLCFVYPLDFARTRLADVKGAGEREFRGLDGLVYTKSDGIRGLYQGFNS 180
 QY 181 VGGIIIRAAVFGVYDTAKGMLDPKNTHTIVSMIAQYTAAGVSYFEDVRRRRMM 240
 Db 181 VGGIIIRAAVFGVYDTAKGMLDPKNTHTIVSMIAQYTAAGVSYFEDVRRRRMM 240
 QY 241 QSGRKADIMYTGTVDCWKRIFRDEGGAFFKGAWSNVLRMGAFVLYLYDELK 296
 Db 241 QSGRKADIMYTGTVDCWKRIFRDEGGAFFKGAWSNVLRMGAFVLYLYDELK 296
 RESULT 9
 AAU10379
 ID AAU10379 standard; Protein; 298 AA.
 AC AAU10379;
 XX 14-FEB-2002 (first entry)
 DE Human adenine nucleotide translocator 2 (ANT2).
 XX
 KW Human; adenine nucleotide translocator; ANT; ss;
 KM mitochondrial matrix protein.
 XX
 OS Homo sapiens.
 XX
 PN WO200185944-A2.
 PD 15-NOV-2001.
 PF 11-MAY-2001; 2001WO-US15416.
 PR 11-MAY-2000; 2000US-0569327.
 PA (MITO-) MITOKOR.
 PI Anderson CM, Davis RE, Cleverger W, Wiley SE, Miller SW, Szabo TR;
 PI Ghosh SS, Moos WH, Pei Y, Carroll AK;
 DR MPI; 2002-055598/07.
 XX N-PSDB; AAS16689.
 PT Novel recombinant expression construct for producing adenine nucleotide
 PT translocator polypeptides, comprises a regulated promoter linked to
 PT nucleic acid encoding the polypeptide -
 XX
 PS Claim 44; Fig 2; 147pp; English.
 CC The invention relates to a recombinant expression construct (I)
 CC comprising a regulated promoter operably linked to a nucleic acid
 CC encoding an adenine nucleotide translocator (ANT) polypeptide. ANT
 CC proteins mediate the exchange of ATP synthesised in the mitochondrial
 CC matrix for ADP in the cytosol. (I) is useful for producing recombinant
 CC ANT polypeptide by transforming a prokaryotic or eukaryotic host cell and
 CC culturing the host cell. (I) is also useful for targeting a polypeptide

CC of interest to a mitochondrial membrane, where ANT polypeptide is
 CC expressed as a fusion protein with the polypeptide of interest.
 CC Recombinant ANT polypeptide, or cells expressing the polypeptide, is
 CC useful for identifying an agent that binds to an ANT polypeptide. ANT
 CC ligand is useful for determining the presence of an ANT polypeptide.
 CC preferably AN1, AN2 or AN3 in a biological sample and for isolating
 CC ANT from a biological sample, where the ANT ligand is covalently or non-
 CC covalently bound to a solid phase. Detectably labeled ANT ligand is also
 CC useful for identifying an agent that interacts with an ANT polypeptide.
 CC The present sequence represents the amino acid sequence of human AN2.
 CC
 XX
 SO Sequence 298 AA:
 Query Match 94.2%; Score 1454; DB 23; Length 298;
 Best Local Similarity 92.6%; Pred. No. 1.7e-147;
 Matches 274; Conservative 13; Mismatches 9; Indels 0; Gaps 0;
 QY 1 MTEQATSFADKDFLAGIAAISKTAAPIERKLLQVQHAHQIAADQYGYDVCYR 60
 DB 1 MTDALSFADKDFLAGIAAISKTAAPIERKLLQVQHAHQIAADQYGYDVCYR 60
 QY 61 IPKEGVLSFMRGNLANVIRYPTQALNFAFDKTKQITLGVDKHTQFWRFFAGNLASG 120
 DB 61 IPKEGVLSFMRGNLANVIRYPTQALNFAFDKTKQITLGVDKHTQFWRFFAGNLASG 120
 QY 121 GAAGATSLCFEYVPDLPFARTRLAADVKGSGTEREFGDGLCVKTKSDGIRGLYGFYSV 180
 DB 121 GAAGATSLCFEYVPDLPFARTRLAADVKGSGTEREFGDGLCVKTKSDGIRGLYGFYSV 180
 QY 181 VOGIIIRAAAYFGVDTAKGMLPDPKNTIIVSWIAQVTVAVAGVSTPFTVRRMM 240
 DB 181 VOGIIIRAAAYFGVDTAKGMLPDPKNTIIVSWIAQVTVAVAGVSTPFTVRRMM 240
 QY 241 QSGRKADIMYTGVDCKRKIFRDEGKAFEGKANSNVLRGGAFLVLYDELK 296
 DB 241 QSGRKADIMYTGVDCKRKIFRDEGKAFEGKANSNVLRGGAFLVLYDELK 296
 RESULT 10
 ABR41715
 ID ABR41715 standard; Protein: 429 AA.
 AC ABR41715;
 XX
 XX 02-JUN-2003 (first entry)
 DE Human DITHP organelle-associated protein.
 KW Human; dithp; diagnostic and therapeutic polynucleotide; diagnosis;
 KW cancer; cell proliferative disorder; autoimmune disorder;
 KW inflammatory disorder; infection; hormonal disorder; metabolic disorder;
 KW neurological disorder; gastrointestinal disorder; transport disorder;
 KW connective tissue disorder; drug screening; proteome analysis;
 KW gene therapy; antisense therapy; genotyping; transgenic animal; knock in;
 KW disease model; toxicological testing; transcript imaging;
 KW organelle-associated protein.
 XX
 OS Homo sapiens.
 XX
 XX WO200297031-A2.
 PN
 XX
 PD 05-DEC-2002.
 PF
 XX 27-MAR-2002; 2002MO-US10056.
 PR 28-MAR-2001; 2001US-279619P.
 PR 29-MAR-2001; 2001US-280067P.
 PR 29-MAR-2001; 2001US-280068P.
 PR 16-MAY-2001; 2001US-291280P.
 PR 17-MAY-2001; 2001US-291829P.
 PR 17-MAY-2001; 2001US-291849P.
 PR 19-JUN-2001; 2001US-299428P.
 PR 20-JUN-2001; 2001US-299776P.

PR 20-JUN-2001; 2001US-300001P.
 XX
 XX (INCY-) INCYTE GENOMICS INC.
 PA
 PI Daffo A, Jones AL, Tran AB, Dahl CR, Gietzen D, Chinn J;
 PI Dufour GE, Hillman JL, Yu JY, Tuason O, Yap PE, Amshay SR;
 PI Daugherty SC, Dam TH, Liu TF, Nguyen DA, Kleeferd Y, Gerstein EH;
 PI Peralta CH, David MR, Lewis SA, Chen AJ, Panzer SR, Harris B;
 PI Flores V, Marwaha R, Lo A, Lan RX, Urashka ME;
 XX
 DR MPI: 2003-129518/12.
 DR N-PSDB; ACC46652.
 XX
 PT Novel human diagnostic and therapeutic polypeptide useful for
 PT identifying test compound which specifically binds to a polypeptide
 PT encoded by human diagnostic and therapeutic polynucleotide, and to
 PT induce antibodies
 PS Claim 27; SEQ ID NO 1250; 591bp; English.
 XX
 CC The invention relates to novel human diagnostic and therapeutic
 CC polynucleotides designated dithp (ACC46080-ACC46749) and to their
 CC encoded proteins (DITHP; ABR41136-ABR41812). The invention also relates
 CC to polynucleotide sequences at least 90% identical to the dithp cDNA
 CC sequences of the invention; recombinant vectors, host cells and
 CC transgenic organisms comprising a dithp nucleic acid sequence; the
 CC recombinant production of DITHP proteins; antibodies specific for DITHP
 CC proteins; microarrays comprising dithp nucleic acid sequences; methods
 CC of detecting dithp nucleotide and protein sequences; methods of screening
 CC for compounds which specifically bind a DITHP protein; and methods of
 CC assessing the toxicity of test compounds using a dithp hybridisation
 CC probe. Dithp nucleic acid sequences and DITHP proteins may be used in the
 CC diagnosis of a wide variety of conditions including cancer and other cell
 CC proliferative disorders; autoimmune or inflammatory disorders; bacterial,
 CC viral, fungal or parasitic infections; hormonal disorders; metabolic
 CC disorders; neurological disorders; gastrointestinal disorders; transport
 CC disorders; and connective tissue disorders. They may also be used to
 CC screen for modulators of protein activity or gene expression. DITHP
 CC proteins can additionally be used in analysis of the proteome of a tissue
 CC or cell type and to induce antibodies. The dithp nucleic acids are
 CC additionally useful in somatic or germline gene therapy of the disorders
 CC mentioned above, as a source of antisense sequences, as a source of
 CC probes and primers, in genotyping and identification of individuals, in
 CC the generation of transgenic animal models of human disease or knock in
 CC humanised animals, in toxicological testing, and in transcript imaging.
 CC The present sequence represents a DITHP protein which is an organelle-
 CC associated protein.
 CC Note: The sequence data for this patent did not form part of the printed
 CC specification, but was obtained in electronic format directly from WIPO
 CC at ftp.wipo.int/pub/published_pot_sequences.
 XX
 SO Sequence 429 AA:
 Query Match 91.9%; Score 1418; DB 24; Length 429;
 Best Local Similarity 95.2%; Pred. No. 2e-143;
 Matches 277; Conservative 3; Mismatches 5; Indels 6; Gaps 2;
 QY 1 MTEQATSFADKDFLAGIAAISKTAAPIERKLLQVQHAHQIAADQYGYDVCYR 60
 DB 26 MTEQATSFADKDFLAGIAAISKTAAPIERKLLQVQHAHQIAADQYGYDVCYR 85
 QY 61 IPKEGVLSFMRGNLANVIRYPTQALNFAFDKTKQITLGVDKHTQFWRFFAGNLASG 120
 DB 86 IPKEGVLSFMRGNLANVIRYPTQALNFAFDKTKQITLGVDKHTQFWRFFAGNLASG 145
 QY 121 GAAGATSLCFEYVPDLPFARTRLAADVKGSGTEREFGDGLCVKTKSDGIRGLYGFYSV 180
 DB 146 GAAGATSLCFEYVPDLPFARTRLAADVKGSGTEREFGDGLCVKTKSDGIRGLYGFYSV 205
 QY 181 VOGIIIRAAAYFGVDTAKGMLPDPKNTIIVSWIAQVTVAVAGVSTPFTVRRMM 240
 DB 206 VOGIIIRAAAYFGVDTAKGMLPDPKNTIIVSWIAQVTVAVAGVSTPFTVRRMM 265

QY 125 ATSLCFVYPLDFAFTRRLADYVKGSGTEREFGDGLVKTIRKSDGIRGLYOGFSVSGCI 184
 DB 121 ATSLCFVYPLDFAFTRRLADYVKGSGTEREFGDGLVKTIRKSDGIRGLYOGFSVSGCI 180
 QY 185 IYRAAYGVYDTAKGMLPDPKNTIHVSMIAQVTAVAGVSYPTPTVRRMMQSGR 244
 DB 181 IYRAAYGVYDTAKGMLPDPKNTIHVSMIAQSVTVAGVSYPTPTVRRMMQSGR 240
 QY 245 KGADIMYGTVDCAWKIRFDEGKAFKFGAMSNTVRGKGAFVLYLDELKK 296
 DB 241 KGADIMYGTVDCAWKIRKAKDEGANAFKFGAMSNTVRGKGAFVLYLDELKK 292

RESULT 13
 AAY71031
 ID AAY71031 standard; Protein: 297 AA.
 AC AAY71031;
 DT 29-AUG-2000 (first entry)
 DE Human adenine nucleotide translocator AMT1.
 XX Human; adenine nucleotide translocator; AMT1; mitochondria; ADP; ATP;
 KM adenosine di-phosphate; adenosine tri-phosphate; apoptosis; MPT; cancer;
 KM mitochondrial permeability transition; neuroprotective; neurotropic;
 KM antiParkinsonian; cytosolitic; antidiabetic; anticonvulsant; neuroleptic;
 KM antiparkinsonic; cerebroprotective; therapeutic; screening; psoriasis;
 KM Alzheimer's disease; Parkinson's disease; Huntington's disease; dystonia;
 KM diabetes; Leber's hereditary optic neuropathy; schizophrenia; MELAS;
 KM mitochondrial encephalopathy; lactic acidosis; stroke; MIDD;
 KM mitochondrial diabetes and deafness; hyperproliferative disorder;
 KM myoclonic epilepsy red ragged fibre syndrome.
 XX Homo sapiens.
 OS WO200026370-A2.
 PN 11-MAY-2000.
 PD 03-NOV-1999; 99WO-US25883.
 XX 03-NOV-1998; 98US-0185904.
 PR 08-SEP-1999; 99US-0393441.
 XX (MITO-) MITOKOR.
 PA
 XX
 PI Anderson CM, Davis RE, Clevenger W, Wiley SE, Miller SW, Szabo TR;
 PI Ghosh SS;
 DR WPI: 2000-365619/31.
 DR N-PSDB: AAD00519.
 XX
 PT Recombinant construct encoding adenine nucleotide translocator
 PT polypeptide, useful e.g. in screening for potential therapeutic agents
 XX against mitochondrial disease -
 XX
 PS Claim 44; Page 172; 175pp; English.

CC disorders, mitochondrial diabetes and deafness (MIDD), and myoclonic
 CC epilepsy red ragged fibre syndrome. The present sequence is an
 CC adenine nucleotide translocator AMT1 from human brain.
 XX

SEQ Sequence 297 AA:
 Query Match 89.8%; Score 1385.5; DB 21; Length 297;
 Best Local Similarity 87.2%; Pred. No. 3.8e-140;
 Matches 260; Conservative 21; Mismatches 16; Indels 1; Gaps 1;

QY 1 MTEQAISFEKADFLAGIAAISKTAAPIERVKLLQVQHASQIADKQYKGIYDCIVR 60
 DB 1 MGDHMSFLKDFLAGAANAASVSTAPPIERVKLLQVQHASQIASEKQYGIIDCYVR 60
 QY 61 IPKEGVLSFWRGNLANVRYRPTQALNFAFDKXKQITLGGVDKHTQWRFPAGNLASG 120
 DB 61 IPKEGVLSFWRGNLANVRYRPTQALNFAFDKXKQITLGGVDKHTQWRFPAGNLASG 120
 QY 121 GAAGATSLCFVYPLDFAFTRRLADYVKGSGTEREFGDGLVKTIRKSDGIRGLYOGFSVS 180
 DB 121 GAAGATSLCFVYPLDFAFTRRLADYVKGSGTEREFGDGLVKTIRKSDGIRGLYOGFSVS 179
 QY 181 VGGIIYRAAYGVYDTAKGMLPDPKNTIHVSMIAQVTAVAGVSYPTPTVRRMMQ 240
 DB 181 VGGIIYRAAYGVYDTAKGMLPDPKNTIHVSMIAQSVTVAGVSYPTPTVRRMMQ 239
 QY 241 OSGRGADIMYGTVDCAWKIRFDEGKAFKFGAMSNTVRGKGAFVLYLDELKKVY 298
 DB 241 OSGRGADIMYGTVDCAWKIRKAKDEGANAFKFGAMSNTVRGKGAFVLYLDELKKVY 297

RESULT 14
 AAU01198
 ID AAU01198 standard; Protein: 297 AA.
 AC AAU01198;
 DT 07-SEP-2001 (first entry)
 DE Human adenine nucleotide translocator-1 (AMT-1) protein.
 XX Human; adenine nucleotide translocator-1; AMT-1; MPT; cyclophilin;
 KM mitochondrial permeability transition pore component; cell survival;
 KM mitochondrial core component; mitochondrial related disorder; cancer;
 KM Alzheimer's disease; diabetes mellitus; hyperproliferative disorder.
 XX Homo sapiens.
 OS WO200132876-A2.
 PN 10-MAY-2001.
 PD 03-NOV-2000; 2000WO-US30535.
 XX 03-NOV-1999; 99US-0434354.
 PR (MITO-) MITOKOR.
 PA
 XX
 PI Murphy AN, Clevenger W, Wiley SE, Andreyev AV, Fritgerl LG;
 PI Velicelebi G, Davis RE;
 DR WPI: 2001-291054/30.
 DR N-PSDB: AAS05901.
 XX
 PT New nucleic acid expression constructs, useful for screening for agents
 PT that alter mitochondrial permeability transition (MPT), comprises
 PT polynucleotide encoding MPT polypeptide or cyclophilin polypeptide
 XX fused to energy transfer molecule -
 XX
 PS Disclosure; Fig 2; 186pp; English.
 CC The present sequence represents human adenine nucleotide translocator-1
 CC (AMT-1) protein. AMT proteins are mitochondrial permeability


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RESULT 2
US-09-434-354-48
; Sequence 48, Application US/09434354
; Patent No. 6562563
; GENERAL INFORMATION:
; APPLICANT: Murphy, Anne N.
; APPLICANT: Clevenger, William
; APPLICANT: Wiley, Sandra Eileen
; APPLICANT: Andreyev, Alexander Y.
; APPLICANT: Frigel, Luciano G.
; APPLICANT: Velicel, Gonul
; APPLICANT: Davis, Robert E.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETERMINING
; TITLE OF INVENTION: INTERACTIONS OF MITOCHONDRIAL COMPONENTS, AND FOR
; FILE REFERENCE: IDENTIFYING AGENTS THAT ALTER SUCH INTERACTIONS
; FILE REFERENCE: 660088.433
; CURRENT APPLICATION NUMBER: US/09/434,354
; CURRENT FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 48
; LENGTH: 298
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-434-354-48

Query Match          94.2%; Score 1454; DB 4; Length 298;
Best Local Similarity 92.6%; Pred. No. 5,2e-156;
Matches 274; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

QY 1 MTEOATSPAKDFLAGGIAAISTKTAAPLIERVKLLQOVHASKQIADKQYKIVDCIVR 60
DB 1 MTEOATSPAKDFLAGGIAAISTKTAAPLIERVKLLQOVHASKQIADKQYKIVDCIVR 60
QY 61 IPKQGVLSFRGNLANVIRYPTQALNFAFKKYOIFLGVDKHTQFRRYRAGNLSG 120
DB 61 IPKQGVLSFRGNLANVIRYPTQALNFAFKKYOIFLGVDKHTQFRRYRAGNLSG 120
QY 121 GAAGATSLCFVYLPDFARTFLADAVGKSTGERFRLGDCLVKITSQIRGLYOGFSVS 180
DB 121 GAAGATSLCFVYLPDFARTFLADAVGKSTGERFRLGDCLVKITSQIRGLYOGFSVS 180
QY 181 VGGIITIRAYFVYTPAKGMLDPKNTHTIVSMIAQVTAAGVSYFDFVRRMM 240
DB 181 VGGIITIRAYFVYTPAKGMLDPKNTHTIVSMIAQVTAAGVSYFDFVRRMM 240
QY 241 QSGRKADIMYTGTCVDCMRKIFRDEGKAFKFGAMSVNLGKGAFVLYLDEIKR 296
DB 241 QSGRKADIMYTGTCVDCMRKIFRDEGKAFKFGAMSVNLGKGAFVLYLDEIKR 296

RESULT 3
US-08-961-871-10
; Sequence 10, Application US/08961871
; Patent No. 6013858
; GENERAL INFORMATION:
; APPLICANT: Wallace, Douglas C.
; APPLICANT: Clevenger, William
; APPLICANT: Wiley, Sandra Eileen
; APPLICANT: Andreyev, Alexander Y.
; APPLICANT: Frigel, Luciano G.
; APPLICANT: Velicel, Gonul
; APPLICANT: Davis, Robert E.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETERMINING
; TITLE OF INVENTION: INTERACTIONS OF MITOCHONDRIAL COMPONENTS, AND FOR
; FILE REFERENCE: IDENTIFYING AGENTS THAT ALTER SUCH INTERACTIONS
; FILE REFERENCE: 660088.433
; CURRENT APPLICATION NUMBER: US/09/434,354
; CURRENT FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 48
; LENGTH: 298
; TYPE: PRT
; ORGANISM: Homo sapien
US-08-961-871-10

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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/961,871
FILING DATE: 01-NOV-1996
ATTORNEY/AGENT INFORMATION:
NAME: Ferber, Donna M.
REGISTRATION NUMBER: 33,878
REFERENCE/DOCKET NUMBER: 78-96
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 499-8080
TELEFAX: (303) 499-8089
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 298 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-961-871-10

Query Match          91.5%; Score 1412; DB 3; Length 298;
Best Local Similarity 88.6%; Pred. No. 2,9e-151;
Matches 264; Conservative 19; Mismatches 15; Indels 0; Gaps 0;

QY 1 MTEOATSPAKDFLAGGIAAISTKTAAPLIERVKLLQOVHASKQIADKQYKIVDCIVR 60
DB 1 MTEOATSPAKDFLAGGIAAISTKTAAPLIERVKLLQOVHASKQIADKQYKIVDCIVR 60
QY 61 IPKQGVLSFRGNLANVIRYPTQALNFAFKKYOIFLGVDKHTQFRRYRAGNLSG 120
DB 61 IPKQGVLSFRGNLANVIRYPTQALNFAFKKYOIFLGVDKHTQFRRYRAGNLSG 120
QY 121 GAAGATSLCFVYLPDFARTFLADAVGKSTGERFRLGDCLVKITSQIRGLYOGFSVS 180
DB 121 GAAGATSLCFVYLPDFARTFLADAVGKSTGERFRLGDCLVKITSQIRGLYOGFSVS 180
QY 181 VGGIITIRAYFVYTPAKGMLDPKNTHTIVSMIAQVTAAGVSYFDFVRRMM 240
DB 181 VGGIITIRAYFVYTPAKGMLDPKNTHTIVSMIAQVTAAGVSYFDFVRRMM 240
QY 241 QSGRKADIMYTGTCVDCMRKIFRDEGKAFKFGAMSVNLGKGAFVLYLDEIKR 298
DB 241 QSGRKADIMYTGTCVDCMRKIFRDEGKAFKFGAMSVNLGKGAFVLYLDEIKR 298

RESULT 4
US-09-434-354-47
; Sequence 47, Application US/09434354
; Patent No. 6562563
; GENERAL INFORMATION:
; APPLICANT: Murphy, Anne N.
; APPLICANT: Clevenger, William
; APPLICANT: Wiley, Sandra Eileen
; APPLICANT: Andreyev, Alexander Y.
; APPLICANT: Frigel, Luciano G.
; APPLICANT: Velicel, Gonul
; APPLICANT: Davis, Robert E.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR DETERMINING
; TITLE OF INVENTION: INTERACTIONS OF MITOCHONDRIAL COMPONENTS, AND FOR
; FILE REFERENCE: IDENTIFYING AGENTS THAT ALTER SUCH INTERACTIONS
; FILE REFERENCE: 660088.433
; CURRENT APPLICATION NUMBER: US/09/434,354
; CURRENT FILING DATE: 1999-11-03
; NUMBER OF SEQ ID NOS: 54
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 47
; LENGTH: 297
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-434-354-47

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| 1 | PRIOR FILING DATE: | 1998-06-17 |
| 2 | PRIOR APPLICATION NUMBER: | 60/089592 |
| 3 | PRIOR FILING DATE: | 1998-06-17 |
| 4 | PRIOR APPLICATION NUMBER: | 60/089600 |
| 5 | PRIOR FILING DATE: | 1998-06-17 |
| 6 | PRIOR APPLICATION NUMBER: | 60/089653 |
| 7 | PRIOR FILING DATE: | 1998-06-17 |
| 8 | PRIOR APPLICATION NUMBER: | 60/089801 |
| 9 | PRIOR FILING DATE: | 1998-06-17 |
| 10 | PRIOR APPLICATION NUMBER: | 60/089907 |
| 11 | PRIOR FILING DATE: | 1998-06-18 |
| 12 | PRIOR APPLICATION NUMBER: | 60/089908 |
| 13 | PRIOR FILING DATE: | 1998-06-18 |
| 14 | PRIOR APPLICATION NUMBER: | 60/089947 |
| 15 | PRIOR FILING DATE: | 1998-06-19 |
| 16 | PRIOR APPLICATION NUMBER: | 60/089948 |
| 17 | PRIOR FILING DATE: | 1998-06-19 |
| 18 | PRIOR APPLICATION NUMBER: | 60/089955 |
| 19 | PRIOR FILING DATE: | 1998-06-19 |
| 20 | PRIOR APPLICATION NUMBER: | 60/090246 |
| 21 | PRIOR FILING DATE: | 1998-06-22 |
| 22 | PRIOR APPLICATION NUMBER: | 60/090255 |
| 23 | PRIOR FILING DATE: | 1998-06-22 |
| 24 | PRIOR APPLICATION NUMBER: | 60/090255 |
| 25 | PRIOR FILING DATE: | 1998-06-22 |
| 26 | PRIOR APPLICATION NUMBER: | 60/090255 |
| 27 | PRIOR FILING DATE: | 1998-06-22 |
| 28 | PRIOR APPLICATION NUMBER: | 60/090349 |
| 29 | PRIOR FILING DATE: | 1998-06-23 |
| 30 | PRIOR APPLICATION NUMBER: | 60/090355 |
| 31 | PRIOR FILING DATE: | 1998-06-23 |
| 32 | PRIOR APPLICATION NUMBER: | 60/090429 |
| 33 | PRIOR FILING DATE: | 1998-06-24 |
| 34 | PRIOR APPLICATION NUMBER: | 60/090431 |
| 35 | PRIOR FILING DATE: | 1998-06-24 |
| 36 | PRIOR APPLICATION NUMBER: | 60/090435 |
| 37 | PRIOR FILING DATE: | 1998-06-24 |
| 38 | PRIOR APPLICATION NUMBER: | 60/090444 |
| 39 | PRIOR FILING DATE: | 1998-06-24 |
| 40 | PRIOR APPLICATION NUMBER: | 60/090445 |
| 41 | PRIOR FILING DATE: | 1998-06-24 |
| 42 | PRIOR APPLICATION NUMBER: | 60/090477 |
| 43 | PRIOR FILING DATE: | 1998-06-24 |
| 44 | PRIOR APPLICATION NUMBER: | 60/090535 |
| 45 | PRIOR FILING DATE: | 1998-06-24 |
| 46 | PRIOR APPLICATION NUMBER: | 60/090540 |
| 47 | PRIOR FILING DATE: | 1998-06-24 |
| 48 | PRIOR APPLICATION NUMBER: | 60/090540 |
| 49 | PRIOR FILING DATE: | 1998-06-24 |
| 50 | PRIOR APPLICATION NUMBER: | 60/090542 |
| 51 | PRIOR FILING DATE: | 1998-06-24 |
| 52 | PRIOR APPLICATION NUMBER: | 60/090557 |
| 53 | PRIOR FILING DATE: | 1998-06-24 |
| 54 | PRIOR APPLICATION NUMBER: | 60/090676 |
| 55 | PRIOR FILING DATE: | 1998-06-25 |
| 56 | PRIOR APPLICATION NUMBER: | 60/090678 |
| 57 | PRIOR FILING DATE: | 1998-06-25 |
| 58 | PRIOR APPLICATION NUMBER: | 60/090690 |
| 59 | PRIOR FILING DATE: | 1998-06-25 |
| 60 | PRIOR APPLICATION NUMBER: | 60/090694 |
| 61 | PRIOR FILING DATE: | 1998-06-25 |
| 62 | PRIOR APPLICATION NUMBER: | 60/090695 |
| 63 | PRIOR FILING DATE: | 1998-06-25 |
| 64 | PRIOR APPLICATION NUMBER: | 60/090696 |
| 65 | PRIOR FILING DATE: | 1998-07-01 |
| 66 | PRIOR APPLICATION NUMBER: | 60/090690 |
| 67 | PRIOR FILING DATE: | 1998-07-01 |
| 68 | PRIOR APPLICATION NUMBER: | 60/091478 |
| 69 | PRIOR FILING DATE: | 1998-07-02 |
| 70 | PRIOR APPLICATION NUMBER: | 60/091544 |
| 71 | PRIOR FILING DATE: | 1998-07-01 |
| 72 | PRIOR APPLICATION NUMBER: | 60/091519 |
| 73 | PRIOR FILING DATE: | 1998-07-02 |

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|-----------------------|--------|--------------------|--------|-----------------|
| Query Match | 20.3%; | Score 314; | DB 4; | Length 469; |
| Best Local Similarity | 30.1%; | Pred. No. 7.8e-27; | | |
| Matches | 89; | Conservative | 60; | Mismatches 115; |
| | | | Indels | 32; |
| | | | Gaps | 11; |

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QY      70  EWGNTLVNIIRFEPTQALNFAPKDYKQIETLGVGVDKHTQEMRYRAGNVLASGGAATSLC 129
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db      242  LMRGNINIVLKTAPEAISIKFMAVEOIKR--LVGSPQET---LRHERLVAGSLGALIAQS 296
QY      130  FYVPLDFARTRLAADVQKSGTERERGRGDCLVKTTSDDGRGLGYQSFVSYGIIITYRA 189
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db      297  SIIPEVLKTRMA--LRKTG---QSGMDCARRLAREGAALFYKGIIVPMIGIITYAG 351
QY      190  AYEGVYDTAKG-----LPDPKNTIIIVYSWMLAQTVTVAVG--VYSPEFDYRRRMNM 240
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
Db      352  IDLAVYETLKNAMLGHVAYNASADPG---VFLLACGTMSSTCGQLASPLVALVRYMQA 407
QY      241  QSGRKADILMYGYDVCWKRIIPRDGCAAFPGKMASNVLBRMGAPV--LVLYDELK 295
      |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||  |||
QY      408  QASIEAPAEPTWSSL--FHHILRTGAGELVGRGLAPNEMKATIPAVYSIYVYELMK 461

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RESULT 6
US-09-188-930-339
Sequence 339, Application US/09188930A
Patent No. 6150502
GENERAL INFORMATION:
APPLICANT: Watson, James D.
APPLICANT: Strachan, Lorna
APPLICANT: Sleeman, Matthew
APPLICANT: Onrust, Rene
APPLICANT: Murlson, James Greg
TITLE OF INVENTION: Compositions Isolated From Skin Cells
TITLE OF INVENTION: and Methods For Their Use
FILE REFERENCE: 11000.1011c1
CURRENT APPLICATION NUMBER: US/09/188,930A
CURRENT FILING DATE: 1998-11-09
NUMBER OF SEQ ID NOS: 348
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 339
LENGTH: 469
TYPE: PR1
ORGANISM: Mouse
US-09-188-930-339

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[illegible]

Db 297 STYMEVLKTRMA--LRKTG---QYSGMLDCARILAKEGVAAATYKGIIPNMLGIIPYAG 351
 QY 190 AYFGVYDTAKGMLDPKNTHTI-----VYSWMIAGTAVTAG--VVSYPEDTVRRR 237
 Db 352 IDLAVETL-----KNFWLQRYAVNSADGCVFVLLACGIISSCGGLASYPALAVTR 404
 QY 238 MMOSGRKADIMTGTVDCKRKIFRDEGKAFKGAWSNVLKRGNGAFV-LVLYDELK 295
 Db 405 MQAQASIEGAEVETWSSL--FKQILRTGEGAFGLYRGLAPNFMKVIPAVSISVYVENLK 461

RESULT 7

US-09-312-283C-339
 ; Sequence 339, Application US/09312283C
 ; Patent No. 6573095
 ; GENERAL INFORMATION:
 ; APPLICANT: Watson, James D.
 ; APPLICANT: Strachan, Lorna
 ; APPLICANT: Sleeman, Matthew
 ; APPLICANT: Onrust, Rene
 ; APPLICANT: Murison, James G.
 ; APPLICANT: Kumble, Krishanand D.
 ; TITLE OF INVENTION: Compositions Isolated from Skin Cells
 ; FILE REFERENCE: 11000.1011C2
 ; CURRENT FILING DATE: US/09/312, 283C
 ; CURRENT FILING DATE: 1999-05-14
 ; NUMBER OF SEQ ID NOS: 425
 ; SOFTWARE: FastSeq for Windows Version 4.0
 ; SEQ ID NO 339
 ; LENGTH: 469
 ; TYPE: PRT
 ; ORGANISM: Mouse
 ; US-09-312-283C-339

Query Match 20.2%; Score 311; DB 4; Length 469;
 Best Local Similarity 29.4%; Pred. No. 1.7e-26;
 Matches 88; Conservative 62; Mismatches 11; Indels 38; Gaps 11;

QY 10 KDFLAGIAAISKTAIVAPIERVKLLQVOHASKOIADKQYKGIIVDCIVIRPKRGVLS 69
 Db 188 RHLYAGGAGAVSRCTPDLRLKYLMOY-HASR-----SNMCIVGFTQIRREGAKS 241
 QY 70 FWRGNLANVIRYFPTQALNFAFKDKYKQIFLGVDKHTQFWRYFAGNLASGGAGATSLC 129
 Db 242 LMRGNINVLKIAPESAIKFMAEQMKR--LVGSDQET---LRHERLVAGSLAGAIKOS 296
 QY 130 FVYPLDPARTLADVGSSTGERFRGLGDCLVKTKSDGIRGLYQGSVSYSQGIITIRA 189
 Db 297 STYMEVLKTRMA--LRKTG---QYSGMLDCARILAKEGVAAATYKGIIPNMLGIIPYAG 351
 QY 190 AYFGVYDTAKGMLDPKNTHTI-----VYSWMIAGTAVTAG--VVSYPEDTVRRR 237
 Db 352 IDLAVETL-----KNFWLQRYAVNSADGCVFVLLACGIISSCGGLASYPALAVTR 404
 QY 238 MMOSGRKADIMTGTVDCKRKIFRDEGKAFKGAWSNVLKRGNGAFV-LVLYDELK 295
 Db 405 MQAQASIEGAEVETWSSL--FKQILRTGEGAFGLYRGLAPNFMKVIPAVSISVYVENLK 461

RESULT 8

US-09-482-273-118
 ; Sequence 118, Application US/09482273
 ; Patent No. 6534631
 ; GENERAL INFORMATION:
 ; APPLICANT: Rosen et al.
 ; TITLE OF INVENTION: 71 Human Secreted Proteins
 ; FILE REFERENCE: P2030P1
 ; CURRENT FILING DATE: US/09/482, 273
 ; CURRENT FILING DATE: 2000-01-13
 ; EARLIER APPLICATION NUMBER: PCT/US99/15849
 ; EARLIER FILING DATE: 1999-07-14
 ; EARLIER APPLICATION NUMBER: 60/092,921

; EARLIER FILING DATE: 1998-07-15
 ; EARLIER APPLICATION NUMBER: 60/092,922
 ; EARLIER FILING DATE: 1998-07-15
 ; EARLIER APPLICATION NUMBER: 60/092,956
 ; EARLIER FILING DATE: 1998-07-15
 ; NUMBER OF SEQ ID NOS: 267
 ; SOFTWARE: PatentIn Ver. 2.0
 ; SEQ ID NO 118
 ; LENGTH: 335
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; NAME/KEY: SITE
 ; LOCATION: (335)
 ; OTHER INFORMATION: Xaa equals stop translation
 ; US-09-482-273-118

Query Match 18.5%; Score 286; DB 4; Length 335;
 Best Local Similarity 29.0%; Pred. No. 6.9e-24;
 Matches 87; Conservative 50; Mismatches 133; Indels 30; Gaps 8;

QY 10 KDFLAGIAAISKTAIVAPIERVKLLQVOHAS-----KOIADKQYKGIIVDCIVIRPK 64
 Db 51 KPFYVGGIASTIAEFGTFPVDLTKRLOYQGSIDARKREL---KTKGHEALFRICKE 106
 QY 65 QGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGVDKHTQFWRYFAGNLASGGAG 124
 Db 107 EGVLLYSGIAPALLRQASYSYGIKIGIYQSLKRLFEVERLEDET-----LLIMWICGVSG 161
 QY 125 ATSLCFVYPLDPARTLADVGSSTGERFRGLGDCLVKTKSDGIRGLYQGSVSYSQGI 184
 Db 162 VISSTIANPTDLKTRMQA---QGSLEFGSMIGS-FIDIYQEGTIRGLMRGVPTAORA 216
 QY 185 IYRAAYEGVYDTAK-----GMLDPKNTHTIYSWMIAGTAVAGVVSYPEDTVRRR 238
 Db 217 AIYVGEVLPYDITTKHLILSGMGDTIITHVVSF---TCGLAGALASNYDVYVTRRM 272
 QY 239 MMOSGRKADIMTGTVDCKRKIFRDEGKAFKGAWSNVLKRGNGAFV-LVLYDELK 297
 Db 273 MNQRAIVGHVDLYKGTVDQILMMWKEHGFALYKGFPMWMLGLGPNWNIIFTYTRDQKRL 332

RESULT 9

US-09-501-558-2
 ; Sequence 2, Application US/09501558
 ; Patent No. 6403784
 ; GENERAL INFORMATION:
 ; APPLICANT: Turner, C. Alexander Jr.
 ; APPLICANT: Mathur, Brian
 ; APPLICANT: Zambrowicz, Brian
 ; TITLE OF INVENTION: NO. 6403784e1 Human Uncoupling Proteins and
 ; FILE REFERENCE: Lex-0012-USA
 ; CURRENT FILING DATE: Polynucleotides Encoding the Same
 ; CURRENT FILING DATE: US/09/501, 558
 ; NUMBER OF SEQ ID NOS: 4
 ; SOFTWARE: FastSeq for Windows Version 3.0
 ; SEQ ID NO 2
 ; LENGTH: 291
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-501-558-2

Query Match 18.4%; Score 283.5; DB 4; Length 291;
 Best Local Similarity 28.9%; Pred. No. 1.1e-23;
 Matches 87; Conservative 54; Mismatches 129; Indels 31; Gaps 9;

QY 10 KDFLAGIAAISKTAIVAPIERVKLLQVOHAS-----KOIADKQYKGIIVDCIVIRPK 64
 Db 7 KPFYVGGIASTIAEFGTFPVDLTKRLOYQGSIDARKREL---KTKGHEALFRICKE 62
 QY 65 QGVLSFWRGNLANVIRYFPTQALNFAFKDKYKQIFLGVDKHTQFWRYFAGNLASGGAG 124

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Db      63 EGIKALYSGLAPMLKQASTGCTIKIGYOSLKRIFTERPDET-----LPINICGLSG 117
      125 ATSLCEVYPLDFARTRLADVGRSGTEREFGDGLVTKTKSDGIRGLYOGFSVSVOGI 184
      118 VISSTIANPVDVAKIRMOA---QSNITQ--CGMIGNMNIYQOEGTSGMLKGVSLTKORA 172
      185 IYRAAYFGVYDTAK-----GMLPDKNTHIVYSWMIACQTVAAVGVSPEDTVARRM 238
      173 AIYVGVELPYDITKHLILSGMLGDTVYTHFLSSF-----TCGLAGALASNPVDVYRTM 228
      239 MMSG-RKGAADIMYGVDCMRKIFRDEGKAFEGKAMSVNLK-GNGAGAVLVLYDELK 236
      229 MNORVLNDRGCSGTGTGLDCLLQTMKNEFPALYKGFPMWMLRIGPMWNIIFVYEQJLK 288
      297 V 297
      289 L 289
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RESULT 10
US-09-160-119-4
; Sequence 4, Application US/09160119A
; Patent No. 6316219
; GENERAL INFORMATION:
; APPLICANT: KRIEF, STEPHANE
; APPLICANT: SOUCHEP, MICHEL
; APPLICANT: BRILL, ANTOINE
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GH-30985
; CURRENT APPLICATION NUMBER: US/09/160,119A
; CURRENT FILING DATE: 1998-09-24
; EARLIER APPLICATION NUMBER: EP 97402511.6
; EARLIER FILING DATE: 1997-10-23
; EARLIER APPLICATION NUMBER: EP 98401655.0
; EARLIER FILING DATE: 1998-07-02
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 4
; LENGTH: 447
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
; US-09-160-119-4
```

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Query Match      18.1%; Score 280; DB 4; Length 447;
Best Local Similarity 27.1%; Pred. No. 5.1e-23;
Matches 80; Conservative 47; Mismatches 148; Indels 20; Gaps 6;
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QY      4 QATSPAKDLAGGIAAISTAVAPIERVKLLQOVHASKQIADQKGIYDCIVRIKIP 63
      96 QVAESAYRFGLSVAGAVGATVAYPIDLVKTRMONGRSTGSFVGLMYTKNSFCFKVLR 155
      64 EOGVLSFWBGNLANVIRFPTQALNFAFKDKYQIFL---GGVDKHTQFMYRAGNLAG 120
      156 YEGFELGRLQLPOLLGVAPERAKIKLVNDFVDRKMHKDSVP-----LAAETLAG 207
      121 GAAGATSLCEVYPLDFARTRLADVGRSGTEREFGDGLVTKTKSDGIRGLYOGFSVS 180
      208 GCAGGSOVLETFNLEIKIRLQY-AGEITTGPRVSL-----SVYRDLGFFGIYKKAAC 261
      181 VOGIITIRAAVFGVYDTAKGMLDPKNTHTIVYSWMIACQTVAV-AGVSYPTPTVRRRM 239
      262 FLRDIPESALYFPCYAHVKAASFANEDGOVSPGSLLAGIAGMPASLVTPADVIKTR-- 319
      240 MOSGRKADIMYGVDCMRKIFRDEGKAFEGKAMSVNLKRGAGAFVLVLYDEL 294
      320 LOYAAARAGOTTYTSGVIDCFRKILREBGPALMKAGARVFRSSPQGVTLITLTEL 374
      Db
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RESULT 11
US-09-160-119-2
; Sequence 2, Application US/09160119A
; Patent No. 6316219
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; GENERAL INFORMATION:
; APPLICANT: KRIEF, STEPHANE
; APPLICANT: SOUCHEP, MICHEL
; APPLICANT: BRILL, ANTOINE
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GH-30985
; CURRENT APPLICATION NUMBER: US/09/160,119A
; CURRENT FILING DATE: 1998-09-24
; EARLIER APPLICATION NUMBER: EP 97402511.6
; EARLIER FILING DATE: 1997-10-23
; EARLIER APPLICATION NUMBER: EP 98401655.0
; EARLIER FILING DATE: 1998-07-02
; NUMBER OF SEQ ID NOS: 4
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 674
; TYPE: PRT
; ORGANISM: HOMO SAPIENS
; US-09-160-119-2
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Query Match      18.1%; Score 280; DB 4; Length 674;
Best Local Similarity 27.1%; Pred. No. 9.4e-23;
Matches 80; Conservative 47; Mismatches 148; Indels 20; Gaps 6;
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QY      4 QATSPAKDLAGGIAAISTAVAPIERVKLLQOVHASKQIADQKGIYDCIVRIKIP 63
      323 QVAESAYRFGLSVAGAVGATVAYPIDLVKTRMONGRSTGSFVGLMYTKNSFCFKVLR 382
      64 EOGVLSFWBGNLANVIRFPTQALNFAFKDKYQIFL---GGVDKHTQFMYRAGNLAG 120
      383 YEGFELGRLQLPOLLGVAPERAKIKLVNDFVDRKMHKDSVP-----LAAETLAG 434
      121 GAAGATSLCEVYPLDFARTRLADVGRSGTEREFGDGLVTKTKSDGIRGLYOGFSVS 180
      435 GCAGGSOVLETFNLEIKIRLQY-AGEITTGPRVSL-----SVYRDLGFFGIYKKAAC 488
      181 VOGIITIRAAVFGVYDTAKGMLDPKNTHTIVYSWMIACQTVAV-AGVSYPTPTVRRRM 239
      489 FLRDIPESALYFPCYAHVKAASFANEDGOVSPGSLLAGIAGMPASLVTPADVIKTR-- 546
      240 MOSGRKADIMYGVDCMRKIFRDEGKAFEGKAMSVNLKRGAGAFVLVLYDEL 294
      547 LOYAAARAGOTTYTSGVIDCFRKILREBGPALMKAGARVFRSSPQGVTLITLTEL 601
      Db
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RESULT 12
US-09-142-565-2
; Sequence 2, Application US/09142565A
; Patent No. 6187560
; GENERAL INFORMATION:
; APPLICANT: Lee James Beeley
; APPLICANT: Kelly Paine
; APPLICANT: Robert James
; TITLE OF INVENTION: NOVEL COMPOUNDS
; FILE REFERENCE: GH-30002
; CURRENT APPLICATION NUMBER: US/09/142,565A
; CURRENT FILING DATE: 1999-06-30
; EARLIER APPLICATION NUMBER: 9704551.2
; EARLIER FILING DATE: 1997-03-05
; EARLIER APPLICATION NUMBER: 9705614.7
; EARLIER FILING DATE: 1997-03-18
; EARLIER APPLICATION NUMBER: 97305305.1
; EARLIER FILING DATE: 1997-07-16
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 2
; LENGTH: 312
; TYPE: PRT
; ORGANISM: HOMO SAPIEN
; US-09-142-565-2
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Query Match      17.2%; Score 265; DB 3; Length 312;
Best Local Similarity 27.1%; Pred. No. 1.5e-21;
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Matches 82; Conservative 52; Mismatches 145; Indels 24; Gaps 8;

QY 7 SFANDFLAGIAAISKTAAPIERVKLLQOV--HASKQIADKQYKIVDCIVRIKRE 64
 DB 12 TMAYFELAGTACADLIFEPDITAKVRLQIQESQGPVATVSADYRGVMGITLMTATEBPR 71
 QY 65 QGVLSFMGNLANVIRYPTQALNFAFKDKYKQIFL-GGVDKHTQFMRYFAGNLAGSGAA 123
 DB 72 EGSPSPYGLVAGLOROMSFASIRIGLYDSVKQYVTPGADNSSLTTRILA-----GCCTT 126
 QY 124 GATSCIFVYPLDEFARTRLAADY--GKSGTEREFGELGDLVKITKSDGIRGLYOGFSVS 181
 DB 127 GAAVTCQOPTDVYKVRQASIHGQPSRSDRKISGTMAYRTIAREEGVRLMKGTLPRT 186
 QY 182 QGIIIRAYFYGYDTAKGMLPDPKNTIIVYSMAIQTYA-----VAGVSYSPDTYRR 236
 DB 187 MRNIVNCAEYVYDILKEKLD---YHLTDNFCHEVSAFAGAFCAFYVASPYDVYKT 243
 QY 237 RMMQSGKRGADIMTGVDCMRKIFRDEGKAFPKGAMSNVLR-GMGAFVLYLYDELK 295
 DB 244 RYM-----NSPPGOYFSPDCKIMKVAQEGPTAFYKGPSPFLRLGSMNVVAFYTYEOLK 298
 QY 296 KVI 298
 DB 299 RAL 301

RESULT 13
 US-08-518-878B-56
 ; Sequence 56, Application US/08518878B
 ; Patent No. 5702902
 ; GENERAL INFORMATION:
 ; APPLICANT: Tartaglia, Louis A.
 ; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
 ; TITLE OF INVENTION: TREATMENT OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
 ; NUMBER OF SEQUENCES: 57
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pennie & Edmonds
 ; STREET: 1155 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: U.S.A.
 ; ZIP: 10036-2711
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/518-878B
 ; FILING DATE: 23-AUG-1995
 ; CLASSIFICATION: 435
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Coruzzi, Laura A.
 ; REGISTRATION NUMBER: 30,742
 ; REFERENCE/DOCKET NUMBER: 7853-036
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (212) 790-9090
 ; TELEFAX: (212) 869-9741/8864
 ; TELEX: 66141 PENNIE
 ; INFORMATION FOR SEQ ID NO: 56:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 299 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: unknown
 ; US-08-518-878B-56

Query Match 16.2%; Score 250.5; DB 1; Length 299;
 Best Local Similarity 24.9%; Pred. No. 6e-20;
 Matches 74; Conservative 52; Mismatches 146; Indels 25; Gaps 8;

QY 12 FLAGIAAISKTAAPIERVKLLQOVHASK--QIADKQYKGIIVDCIVRIKREGVL 68

DB 7 FLAGTACIADLIFEPDITAKVRLQIQESQGPVATVSADYRGVMGITLMTATEBPR 66
 QY 69 SFWRGNLANVIRYPTQALNFAFKDKYKQIFLGGVDKHTQFMRYFAGNLAGSGAATSL 128
 DB 67 SLYNGVLVAGLOROMSFASIRIGLYDSVKQYFKG--SEHAS-----IGSRLLAGSTTGALAV 121
 QY 129 CFVYPLDEFARTRLAADVKGSGTEREFGELGDLVITKSDGIRGLYOGFSVSOGIIYR 188
 DB 122 AVAOPTDVYKVRQAO--ARAGGRRYOSTVNAKTYIAREEGVRLMKGTSPVANAIYN 180
 QY 189 AAFVGYDTAK-----GMLPDPKNTIIVYSMAIQTYAVAGVSYSPDTYRRMMQOS 242
 DB 181 CAELVYDILKIDALKRANLMTDLPCHFSASAGACFTFYIAS---PVDVYKTRYM--- 233
 QY 243 GRKADIMTGVDCMRKIFRDEGKAFPKGAMSNVLR-GMGAFVLYLYDELKRYI 298
 DB 234 --NSALGOYSSAGHCAITMLQKEGPRATYKGPSPFLRLGSMNVVAFYTYELKRAL 288

RESULT 14
 US-08-470-868A-56
 ; Sequence 56, Application US/08470868A
 ; Patent No. 5861485
 ; GENERAL INFORMATION:
 ; APPLICANT: Tartaglia, Louis C.
 ; TITLE OF INVENTION: Compositions and Methods for the
 ; TITLE OF INVENTION: Treatment of Body Weight Disorders, Including Obesity
 ; NUMBER OF SEQUENCES: 56
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Pennie and Edmonds
 ; STREET: 1155 Avenue of the Americas
 ; CITY: New York
 ; STATE: New York
 ; COUNTRY: USA
 ; ZIP: 10036
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Floppy disk
 ; COMPUTER: IBM PC compatible
 ; OPERATING SYSTEM: PC-DOS/MS-DOS
 ; SOFTWARE: Patent Release #1.0, Version #1.30
 ; CURRENT APPLICATION DATA:
 ; APPLICATION NUMBER: US/08/470,868A
 ; FILING DATE: 06-JUN-1995
 ; CLASSIFICATION: 530
 ; ATTORNEY/AGENT INFORMATION:
 ; NAME: Coruzzi, Laura A.
 ; REGISTRATION NUMBER: 30,742
 ; REFERENCE/DOCKET NUMBER: 7853-0031-999
 ; TELECOMMUNICATION INFORMATION:
 ; TELEPHONE: (212) 790-9090
 ; TELEFAX: (212) 869-8864
 ; TELEX: 66441 PENNIE
 ; INFORMATION FOR SEQ ID NO: 56:
 ; SEQUENCE CHARACTERISTICS:
 ; LENGTH: 299 amino acids
 ; TYPE: amino acid
 ; STRANDEDNESS: single
 ; TOPOLOGY: unknown
 ; US-08-470-868A-56

Query Match 16.2%; Score 250.5; DB 2; Length 299;
 Best Local Similarity 24.9%; Pred. No. 6e-20;
 Matches 74; Conservative 52; Mismatches 146; Indels 25; Gaps 8;

QY 12 FLAGIAAISKTAAPIERVKLLQOVHASK--QIADKQYKGIIVDCIVRIKREGVL 68
 DB 7 FLAGTACIADLIFEPDITAKVRLQIQESQGPVATVSADYRGVMGITLMTATEBPR 66
 QY 69 SFWRGNLANVIRYPTQALNFAFKDKYKQIFLGGVDKHTQFMRYFAGNLAGSGAATSL 128
 DB 67 SLYNGVLVAGLOROMSFASIRIGLYDSVKQYFKG--SEHAS-----IGSRLLAGSTTGALAV 121

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0Y      CFVYVLDLPAARTLADVCSGEREREGJDDCLVTKTKDGIJGLVQGSVSNVQJILYR 188
Db      122  AVAOPTDVKKVRFQAO-ARAGGGRKRYOSTVNAIKYITAREEGERGLKGSPPNARAIYN 180
0Y      189  AAFEGVYDTAK-----GMLPDPKNTTHIYVSNMIAQTVAAVGVSVSPEDTVRRMMQOS 242
Db      181  CAELVTYVLIKDALKKANIMTDDLECHFFSAGGAGCTTYIAS----PDVYKTRYM---- 233
0Y      243  GRKGADIMYTGTVDCMRKIFRDEGGKAFFKAGMSNVLK-IGMGAFLVLYVDELKRYI 298
Db      234  --NSMLGGYSSSAGHCLTMLQKEGRRAFYKGMSPSLTRGSMNVNVAFVYIEQLKRAL 288

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OY      243 GRGAGADIMYGTVDYCDKRIKIFRDEGGCAFKGAMSVLVR-GMGGAFFVLVLYDELKKVI 298
Db      244 --NSALQGYSSAGHCALYLMQKEGPRAFYKGMPSFRLNLSMNVMYVFYTYEQLRAL 298
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RESULT 15
 US-08-518-878B-51
 : Sequence 51, Application US/08518878B
 : Patent No. 5702902
 :
 : GENERAL INFORMATION:
 : APPLICANT: Tartaglia, Louis A.
 : TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
 : TREATMENT OF BODY WEIGHT DISORDERS, INCLUDING OBESITY
 : NUMBER OF SEQUENCES: 57
 : CORRESPONDENCE ADDRESS:
 : ADDRESSEE: Pennie & Edmonds
 : STREET: 1155 Avenue of the Americas
 : CITY: New York
 : STATE: New York
 : COUNTRY: U.S.A.
 : ZIP: 10036-2711
 :
 : COMPUTER READABLE FORM:
 : MEDIUM TYPE: Floppy disk
 : COMPUTER: IBM PC compatible
 : OPERATING SYSTEM: PC-DOS/MS-DOS
 : SOFTWARE: Patentin Release #1.0, Version #1.30
 : CURRENT APPLICATION DATA:
 : APPLICATION NUMBER: US/08/518,878B
 : FILING DATE: 23-AUG-1995
 : CLASSIFICATION: 435
 : ATTORNEY/AGENT INFORMATION:
 : NAME: Coruzzi, Laura A.
 : REGISTRATION NUMBER: 30,742
 : REFERENCE/DOCKET NUMBER: 7853-036
 : TELECOMMUNICATION INFORMATION:
 : TELEPHONE: (212) 790-9090
 : TELEFAX: (212) 869-9741/8864
 : TELE: 66141 PENNIE
 : INFORMATION FOR SEQ ID NO: 51:
 : SEQUENCE CHARACTERISTICS:
 : LENGTH: 309 amino acids
 : TYPE: amino acid
 : STRANDEDNESS: single
 : TOPOLOGY: unknown
 : US-08-518-878B-51

| | | | | |
|--------------------------|--------|--------------------|------------|-------------|
| Query Match | 16.28; | Score 250.5; | DB 1; | Length 309; |
| Best Local Similarity | 24.98; | Pred. No. 6.3e-20; | | |
| Matches 74; Conservative | 52; | Mismatches 146; | Indels 25; | Gaps 8 |

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QY 12 FLAGGAAAIISKRAVPIERVLLLOVOHASK---QIADKORYGYDCAIRPEKGYL 68
Db 17 FLGAGTAACTADLTFFPDLTAKVRQIQGESQPPRAATVSAQKGVMTITLTPWRIEGR 76
QY 69 SEWRGNIAVYRYEPTQALNFAEKDKYQIPLGVDKHTQFWRYEAGNLASGGAAGTSL 128
Db 77 SLVNGTVAGIQRMSPASVRIGLYDSVQMFYKQ-SEHAS----IGSRLLAGSTTGALAV 131
QY 129 CFYVPLDEPARTLADAVKSGSTEREERGLGDCLYAKITKSDGIRGLYOGFSVSVOGITTYR 188
Db 132 AVAQPPDVVYKVFQAO-ARAGGGRRYQOSTVNAKYKTIAREEGEFGRLMGKTSPPNARNAIYN 190
QY 189 AAFVGYVDNAK-----GMLDPKNTHTIYVSMNLAQTYTAAGVSVPEPDVYRRRMMQS 242
Db 191 CAELVYVDLIKALLKANLMTDCLDCHHTSASAGACFCTVTIAS---PVDVVKIRYV--- 243

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GenCore version 5.1.6
Copyright (c) 1993 - 2003 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 28, 2003, 19:38:56 ; Search time 19.355 Seconds

(without alignments)
2105.969 Million cell updates/sec

Title: US-09-811-132-33

Perfect score: 1543
Sequence: 1 MTEQAISFADFLAGIAAA.....LRGNGAFVLYDELKRV 298

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 510680 seqs, 136781880 residues

Total number of hits satisfying chosen parameters: 510680

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

Published_Applications_AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/1/pubpaa/PCR_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/1/pubpaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
- 6: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep:*
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- 9: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
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- 11: /cgn2_6/ptodata/1/pubpaa/US09_PUBCOMB.pep:*
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- 13: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/1/pubpaa/US10_PUBCOMB.pep:*
- 17: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep:*
- 18: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|--------|-------------|--------|-------|--------------------|
| 1 | 1543 | 100.0 | 298 | 9 | US-09-811-094-33 |
| 2 | 1543 | 100.0 | 298 | 9 | US-09-810-644-33 |
| 3 | 1543 | 100.0 | 298 | 10 | US-09-185-904A-33 |
| 4 | 1454 | 94.2 | 298 | 9 | US-09-811-094-32 |
| 5 | 1454 | 94.2 | 298 | 9 | US-09-810-644-32 |
| 6 | 1454 | 94.2 | 298 | 10 | US-09-185-904A-32 |
| 7 | 1385.5 | 89.8 | 297 | 9 | US-09-811-094-31 |
| 8 | 1385.5 | 89.8 | 297 | 9 | US-09-810-644-31 |
| 9 | 1385.5 | 89.8 | 297 | 9 | US-09-185-904A-31 |
| 10 | 760.5 | 49.3 | 318 | 10 | US-09-801-368-252 |
| 11 | 749.5 | 48.6 | 386 | 9 | US-09-734-569-170 |
| 12 | 737 | 47.8 | 308 | 15 | US-10-128-714-3338 |
| 13 | 737 | 47.8 | 308 | 15 | US-10-128-714-3338 |
| 14 | 734.5 | 47.6 | 381 | 12 | US-10-141-478A-2 |
| 15 | 686 | 44.5 | 677 | 12 | US-10-259-165-192 |

| | | | | | | |
|----|-------|------|-----|----|---------------------|-------------------|
| 16 | 518 | 33.6 | 132 | 9 | US-09-925-301-1459 | Sequence 1459, Ap |
| 17 | 423 | 27.4 | 87 | 9 | US-09-864-761-36440 | Sequence 36440, A |
| 18 | 368 | 23.8 | 475 | 10 | US-09-777-921A-4 | Sequence 4, Appl1 |
| 19 | 368 | 23.8 | 477 | 10 | US-09-777-921A-2 | Sequence 2, Appl1 |
| 20 | 333.5 | 21.6 | 410 | 10 | US-09-777-921A-5 | Sequence 5, Appl1 |
| 21 | 314 | 20.3 | 469 | 9 | US-09-989-722-289 | Sequence 289, App |
| 22 | 314 | 20.3 | 469 | 9 | US-09-989-722-289 | Sequence 289, App |
| 23 | 314 | 20.3 | 469 | 9 | US-09-989-722-289 | Sequence 289, App |
| 24 | 314 | 20.3 | 469 | 9 | US-09-989-722-289 | Sequence 289, App |
| 25 | 314 | 20.3 | 469 | 10 | US-09-989-721-289 | Sequence 289, App |
| 26 | 314 | 20.3 | 469 | 10 | US-09-989-722-289 | Sequence 289, App |
| 27 | 314 | 20.3 | 469 | 10 | US-09-991-073-289 | Sequence 289, App |
| 28 | 314 | 20.3 | 469 | 10 | US-09-990-442-289 | Sequence 289, App |
| 29 | 314 | 20.3 | 469 | 10 | US-09-991-163-289 | Sequence 289, App |
| 30 | 314 | 20.3 | 469 | 10 | US-09-993-604-289 | Sequence 289, App |
| 31 | 314 | 20.3 | 469 | 10 | US-09-990-456-289 | Sequence 289, App |
| 32 | 314 | 20.3 | 469 | 10 | US-09-988-721-289 | Sequence 289, App |
| 33 | 314 | 20.3 | 469 | 10 | US-09-988-721-289 | Sequence 289, App |
| 34 | 314 | 20.3 | 469 | 10 | US-09-988-721-289 | Sequence 289, App |
| 35 | 314 | 20.3 | 469 | 10 | US-09-988-721-289 | Sequence 289, App |
| 36 | 314 | 20.3 | 469 | 10 | US-09-990-444-289 | Sequence 289, App |
| 37 | 314 | 20.3 | 469 | 10 | US-09-991-181-289 | Sequence 289, App |
| 38 | 314 | 20.3 | 469 | 10 | US-09-988-720-289 | Sequence 289, App |
| 39 | 314 | 20.3 | 469 | 10 | US-09-990-456-289 | Sequence 289, App |
| 40 | 314 | 20.3 | 469 | 10 | US-09-993-687-289 | Sequence 289, App |
| 41 | 314 | 20.3 | 469 | 11 | US-09-989-734-289 | Sequence 289, App |
| 42 | 314 | 20.3 | 469 | 11 | US-09-997-653-289 | Sequence 289, App |
| 43 | 314 | 20.3 | 469 | 11 | US-09-997-653-289 | Sequence 289, App |
| 44 | 314 | 20.3 | 469 | 11 | US-09-997-653-289 | Sequence 289, App |
| 45 | 314 | 20.3 | 469 | 11 | US-09-997-653-289 | Sequence 289, App |

ALIGNMENTS

RESULT 1
US-09-811-094-33
Sequence 33, Appl1
Patent No. US20010044144A1
GENERAL INFORMATION:
APPLICANT: Anderson, Christen M.
APPLICANT: Davis, Robert E.
APPLICANT: Clevenger, William
APPLICANT: Wiley, Sandra Eileen
APPLICANT: Miller, Scott W.
APPLICANT: Szabo, Tomas R.
APPLICANT: Ghosh, Soumitra S.
APPLICANT: Moos, Walter H.
TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),
FILE REFERENCE: 660088.420D4
CURRENT FILING DATE: 2001-03-14
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 33
LENGTH: 298
TYPE: PRT
ORGANISM: Homo sapien
US-09-811-094-33
Query Match 100.0% Score 1543; DB 9; Length 298;
Best Local Similarity 100.0%; Pred. No. 7.6e-157;
Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MTEQAISFADFLAGIAAISKTAIVAPLERKLLQVQHASKOIAADROYGYDCIYR 60
DB 1 MTEQAISFADFLAGIAAISKTAIVAPLERKLLQVQHASKOIAADROYGYDCIYR 60
QY 61 IRKEGVLSFWNGNLANVIRPPTOLANFAFDKTKQITLGVDKHTQWRFPAGNLSG 120
DB 61 IRKEGVLSFWNGNLANVIRPPTOLANFAFDKTKQITLGVDKHTQWRFPAGNLSG 120

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QY      121 GAAGATSLCEVYPLDFARTRLADVGSGTEREERGLGDCLVKTKSDGIRGLYQGSFSVS 180
      121 GAAGATSLCEVYPLDFARTRLADVGSGTEREERGLGDCLVKTKSDGIRGLYQGSFSVS 180
Db      181 VGGIITIRAAVFGVYDPAKGMPLDPKNTHTVSMIAQTYAAVGVSYFPDYVRRRMM 240
      181 VGGIITIRAAVFGVYDPAKGMPLDPKNTHTVSMIAQTYAAVGVSYFPDYVRRRMM 240
QY      241 QSGRKADIMYTGTVDCMRKIFRDEGKAFKFGAMSVNLKMGCAFVLVLYDELKVI 298
      241 QSGRKADIMYTGTVDCMRKIFRDEGKAFKFGAMSVNLKMGCAFVLVLYDELKVI 298
Db      241 QSGRKADIMYTGTVDCMRKIFRDEGKAFKFGAMSVNLKMGCAFVLVLYDELKVI 298

RESULT 2
US-09-810-644-33
; Sequence 33, Application US/09810644
; Patent No. US20020012992A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, Christen M.
; APPLICANT: Davis, Robert E.
; APPLICANT: Clevenger, William
; APPLICANT: Willey, Sandra Eileen
; APPLICANT: Willey, Scott W.
; APPLICANT: Szabo, Tomas R.
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Moos, Walter H.
; APPLICANT: Pel, Yazhong
; TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),
; FILE REFERENCE: 660088.420D3
; CURRENT APPLICATION NUMBER: US/09/810.644
; CURRENT FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 33
; LENGTH: 298
; TYPE: PRT
; ORGANISM: Homo sapien
; US-09-810-644-33

Query Match      100.0%; Score 1543; DB 9; Length 298;
Best Local Similarity 100.0%; Pred. No. 7.6e-157;
Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MTEQAISFADFLAGGIAAISKTAVAPIERVKLLQVHASKQIAADKQKGIYDCIVR 60
      1 MTEQAISFADFLAGGIAAISKTAVAPIERVKLLQVHASKQIAADKQKGIYDCIVR 60
Db      61 IPKQGLSVFWRGLANVIRFPQALNFAFKDKYKQIFLGVDKHTQFRRYFAGNLSG 120
      61 IPKQGLSVFWRGLANVIRFPQALNFAFKDKYKQIFLGVDKHTQFRRYFAGNLSG 120
QY      61 IPKQGLSVFWRGLANVIRFPQALNFAFKDKYKQIFLGVDKHTQFRRYFAGNLSG 120
      61 IPKQGLSVFWRGLANVIRFPQALNFAFKDKYKQIFLGVDKHTQFRRYFAGNLSG 120
Db      121 GAAGATSLCEVYPLDFARTRLADVGSGTEREERGLGDCLVKTKSDGIRGLYQGSFSVS 180
      121 GAAGATSLCEVYPLDFARTRLADVGSGTEREERGLGDCLVKTKSDGIRGLYQGSFSVS 180
QY      121 GAAGATSLCEVYPLDFARTRLADVGSGTEREERGLGDCLVKTKSDGIRGLYQGSFSVS 180
      121 GAAGATSLCEVYPLDFARTRLADVGSGTEREERGLGDCLVKTKSDGIRGLYQGSFSVS 180
Db      181 VGGIITIRAAVFGVYDPAKGMPLDPKNTHTVSMIAQTYAAVGVSYFPDYVRRRMM 240
      181 VGGIITIRAAVFGVYDPAKGMPLDPKNTHTVSMIAQTYAAVGVSYFPDYVRRRMM 240
QY      241 QSGRKADIMYTGTVDCMRKIFRDEGKAFKFGAMSVNLKMGCAFVLVLYDELKVI 298
      241 QSGRKADIMYTGTVDCMRKIFRDEGKAFKFGAMSVNLKMGCAFVLVLYDELKVI 298
Db      241 QSGRKADIMYTGTVDCMRKIFRDEGKAFKFGAMSVNLKMGCAFVLVLYDELKVI 298

RESULT 3
US-09-185-904A-33
; Sequence 33, Application US/09185904A
; Patent No. US2002017185A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, Christen M.
; APPLICANT: Davis, Robert E.

```

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; APPLICANT: Clevenger, William
; APPLICANT: Willey, Sandra Eileen
; APPLICANT: Willey, Scott W.
; APPLICANT: Szabo, Tomas R.
; APPLICANT: Ghosh, Soumitra S.
; TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE
; TITLE OF INVENTION: TRANSLOCATOR (ANT), NOVEL ANT LIGANDS AND SCREENING ASSAYS
; FILE REFERENCE: 660088.420
; CURRENT APPLICATION NUMBER: US/09/185.904A
; CURRENT FILING DATE: 1998-11-03
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 33
; LENGTH: 298
; TYPE: PRT
; ORGANISM: Homo sapien
; US-09-185-904A-33

Query Match      100.0%; Score 1543; DB 10; Length 298;
Best Local Similarity 100.0%; Pred. No. 7.6e-157;
Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY      1 MTEQAISFADFLAGGIAAISKTAVAPIERVKLLQVHASKQIAADKQKGIYDCIVR 60
      1 MTEQAISFADFLAGGIAAISKTAVAPIERVKLLQVHASKQIAADKQKGIYDCIVR 60
Db      61 IPKQGLSVFWRGLANVIRFPQALNFAFKDKYKQIFLGVDKHTQFRRYFAGNLSG 120
      61 IPKQGLSVFWRGLANVIRFPQALNFAFKDKYKQIFLGVDKHTQFRRYFAGNLSG 120
QY      61 IPKQGLSVFWRGLANVIRFPQALNFAFKDKYKQIFLGVDKHTQFRRYFAGNLSG 120
      61 IPKQGLSVFWRGLANVIRFPQALNFAFKDKYKQIFLGVDKHTQFRRYFAGNLSG 120
Db      121 GAAGATSLCEVYPLDFARTRLADVGSGTEREERGLGDCLVKTKSDGIRGLYQGSFSVS 180
      121 GAAGATSLCEVYPLDFARTRLADVGSGTEREERGLGDCLVKTKSDGIRGLYQGSFSVS 180
QY      121 GAAGATSLCEVYPLDFARTRLADVGSGTEREERGLGDCLVKTKSDGIRGLYQGSFSVS 180
      121 GAAGATSLCEVYPLDFARTRLADVGSGTEREERGLGDCLVKTKSDGIRGLYQGSFSVS 180
Db      181 VGGIITIRAAVFGVYDPAKGMPLDPKNTHTVSMIAQTYAAVGVSYFPDYVRRRMM 240
      181 VGGIITIRAAVFGVYDPAKGMPLDPKNTHTVSMIAQTYAAVGVSYFPDYVRRRMM 240
QY      241 QSGRKADIMYTGTVDCMRKIFRDEGKAFKFGAMSVNLKMGCAFVLVLYDELKVI 298
      241 QSGRKADIMYTGTVDCMRKIFRDEGKAFKFGAMSVNLKMGCAFVLVLYDELKVI 298
Db      241 QSGRKADIMYTGTVDCMRKIFRDEGKAFKFGAMSVNLKMGCAFVLVLYDELKVI 298

RESULT 4
US-09-811-094-32
; Sequence 32, Application US/09811094
; Patent No. US2001004414A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, Christen M.
; APPLICANT: Davis, Robert E.
; APPLICANT: Clevenger, William
; APPLICANT: Willey, Sandra Eileen
; APPLICANT: Willey, Scott W.
; APPLICANT: Szabo, Tomas R.
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Moos, Walter H.
; APPLICANT: Pel, Yazhong
; TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLOCATOR (ANT),
; FILE REFERENCE: 660088.420D4
; CURRENT APPLICATION NUMBER: US/09/811.094
; CURRENT FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 32
; LENGTH: 298
; TYPE: PRT
; ORGANISM: Homo sapien
; US-09-811-094-32

Query Match      94.2%; Score 1454; DB 9; Length 298;
Best Local Similarity 92.6%; Pred. No. 2.6e-147;

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Matches 274; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

OY 1 MTEQAISPAKDFLAGGIAAIAISKTAVAPIERVKLLQVOHASKOJTAADKQYKGIYDCIVR 60
1 MTDAALSPAKDFLAGGVAIAISKTAVAPIERVKLLQVOHASKOJTAADKQYKGIYDCIVR 60
OY 61 IPKEQGVLSFWKGNLANVIRFPFOALNFAFKDKYKQJFLGVDKHTQFWRFPAAGNLASG 120
61 IPKEQGVLSFWKGNLANVIRFPFOALNFAFKDKYKQJFLGVDKHTQFWRFPAAGNLASG 120
OY 121 GAAGATSLCFYVPLDFARTRLAADVGKSGTEREFGLDCLVTKIKSGIGLGYGFSVS 180
121 GAAGATSLCFYVPLDFARTRLAADVGKSGTEREFGLDCLVTKIKSGIGLGYGFSVS 180
OY 121 GAAGATSLCFYVPLDFARTRLAADVGKSGTEREFGLDCLVTKIKSGIGLGYGFSVS 180
121 GAAGATSLCFYVPLDFARTRLAADVGKSGTEREFGLDCLVTKIKSGIGLGYGFSVS 180
OY 181 VOGIIIRAAVFGIYDTAKGMLPDPKNTNHIYVSMIAQTVAVAGVSPFDVYRRMM 240
181 VOGIIIRAAVFGIYDTAKGMLPDPKNTNHIYVSMIAQTVAVAGVSPFDVYRRMM 240
OY 241 OSGRKADIMYTGTDCKWKIRFDEGKAFKGAANSNVLKMGAFVLVLYDELK 296
241 OSGRKADIMYTGTDCKWKIRFDEGKAFKGAANSNVLKMGAFVLVLYDELK 296
DB 241 OSGRKGTIDIMYTGTDCKWKIRADEGKAFKGAANSNVLKMGAFVLVLYDELK 296

RESULT 5

US-09-810-644-32
; Sequence 32, Application US/09810644
; Patent No. US20020012992A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, Christen M.
; APPLICANT: Davis, Robert E.
; APPLICANT: Clevenger, William
; APPLICANT: Wiley, Sandra Eileen
; APPLICANT: Willey, Scott W.
; APPLICANT: Szabo, Tomas R.
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Moos, Walter H.
; APPLICANT: Pel, Yehong
; TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLATOR (ANT),
; TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR
; FILE REFERENCE: 660088.420D3
; CURRENT APPLICATION NUMBER: US/09/810,644
; CURRENT FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 37
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 32
; LENGTH: 298
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-810-644-32

Query Match 94.2%; Score 1454; DB 9; Length 298;
Best Local Similarity 92.6%; Pred. No. 2,6e-147;
Matches 274; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

OY 1 MTEQAISPAKDFLAGGIAAIAISKTAVAPIERVKLLQVOHASKOJTAADKQYKGIYDCIVR 60
1 MTDAALSPAKDFLAGGVAIAISKTAVAPIERVKLLQVOHASKOJTAADKQYKGIYDCIVR 60
OY 61 IPKEQGVLSFWKGNLANVIRFPFOALNFAFKDKYKQJFLGVDKHTQFWRFPAAGNLASG 120
61 IPKEQGVLSFWKGNLANVIRFPFOALNFAFKDKYKQJFLGVDKHTQFWRFPAAGNLASG 120
OY 121 GAAGATSLCFYVPLDFARTRLAADVGKSGTEREFGLDCLVTKIKSGIGLGYGFSVS 180
121 GAAGATSLCFYVPLDFARTRLAADVGKSGTEREFGLDCLVTKIKSGIGLGYGFSVS 180
OY 121 GAAGATSLCFYVPLDFARTRLAADVGKSGTEREFGLDCLVTKIKSGIGLGYGFSVS 180
121 GAAGATSLCFYVPLDFARTRLAADVGKSGTEREFGLDCLVTKIKSGIGLGYGFSVS 180
OY 181 VOGIIIRAAVFGIYDTAKGMLPDPKNTNHIYVSMIAQTVAVAGVSPFDVYRRMM 240
181 VOGIIIRAAVFGIYDTAKGMLPDPKNTNHIYVSMIAQTVAVAGVSPFDVYRRMM 240
OY 241 OSGRKADIMYTGTDCKWKIRFDEGKAFKGAANSNVLKMGAFVLVLYDELK 296
241 OSGRKADIMYTGTDCKWKIRFDEGKAFKGAANSNVLKMGAFVLVLYDELK 296
DB 241 OSGRKGTIDIMYTGTDCKWKIRADEGKAFKGAANSNVLKMGAFVLVLYDELK 296

RESULT 6

US-09-185-904A-32
; Sequence 32, Application US/09185904A
; Patent No. US20020177185A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, Christen M.
; APPLICANT: Davis, Robert E.
; APPLICANT: Clevenger, William
; APPLICANT: Wiley, Sandra Eileen
; APPLICANT: Willey, Scott W.
; APPLICANT: Szabo, Tomas R.
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Moos, Walter H.
; APPLICANT: Pel, Yehong
; TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE
; TITLE OF INVENTION: TRANSLATOR (ANT), NOVEL ANT LIGANDS AND SCREENING ASSAYS
; FILE REFERENCE: 660088.420
; CURRENT APPLICATION NUMBER: US/09/185,904A
; CURRENT FILING DATE: 1998-11-03
; NUMBER OF SEQ ID NOS: 33
; SOFTWARE: FastSeq for Windows Version 3.0
; SEQ ID NO 32
; LENGTH: 298
; TYPE: PRT
; ORGANISM: Homo sapien
US-09-185-904A-32

Query Match 94.2%; Score 1454; DB 10; Length 298;
Best Local Similarity 92.6%; Pred. No. 2,6e-147;
Matches 274; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

OY 1 MTEQAISPAKDFLAGGIAAIAISKTAVAPIERVKLLQVOHASKOJTAADKQYKGIYDCIVR 60
1 MTDAALSPAKDFLAGGVAIAISKTAVAPIERVKLLQVOHASKOJTAADKQYKGIYDCIVR 60
OY 61 IPKEQGVLSFWKGNLANVIRFPFOALNFAFKDKYKQJFLGVDKHTQFWRFPAAGNLASG 120
61 IPKEQGVLSFWKGNLANVIRFPFOALNFAFKDKYKQJFLGVDKHTQFWRFPAAGNLASG 120
OY 121 GAAGATSLCFYVPLDFARTRLAADVGKSGTEREFGLDCLVTKIKSGIGLGYGFSVS 180
121 GAAGATSLCFYVPLDFARTRLAADVGKSGTEREFGLDCLVTKIKSGIGLGYGFSVS 180
OY 121 GAAGATSLCFYVPLDFARTRLAADVGKSGTEREFGLDCLVTKIKSGIGLGYGFSVS 180
121 GAAGATSLCFYVPLDFARTRLAADVGKSGTEREFGLDCLVTKIKSGIGLGYGFSVS 180
OY 181 VOGIIIRAAVFGIYDTAKGMLPDPKNTNHIYVSMIAQTVAVAGVSPFDVYRRMM 240
181 VOGIIIRAAVFGIYDTAKGMLPDPKNTNHIYVSMIAQTVAVAGVSPFDVYRRMM 240
OY 241 OSGRKADIMYTGTDCKWKIRFDEGKAFKGAANSNVLKMGAFVLVLYDELK 296
241 OSGRKADIMYTGTDCKWKIRFDEGKAFKGAANSNVLKMGAFVLVLYDELK 296
DB 241 OSGRKGTIDIMYTGTDCKWKIRADEGKAFKGAANSNVLKMGAFVLVLYDELK 296

RESULT 7

US-09-811-094-31
; Sequence 31, Application US/09811094
; Patent No. US20010044144A1
; GENERAL INFORMATION:
; APPLICANT: Anderson, Christen M.
; APPLICANT: Davis, Robert E.
; APPLICANT: Clevenger, William
; APPLICANT: Wiley, Sandra Eileen
; APPLICANT: Willey, Scott W.
; APPLICANT: Szabo, Tomas R.
; APPLICANT: Ghosh, Soumitra S.
; APPLICANT: Moos, Walter H.
; APPLICANT: Pel, Yehong
; TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLATOR (ANT),
; TITLE OF INVENTION: NOVEL ANT LIGANDS AND SCREENING ASSAYS THEREFOR
; FILE REFERENCE: 660088.420D4
; CURRENT APPLICATION NUMBER: US/09/811,094
; CURRENT FILING DATE: 2001-03-14
; NUMBER OF SEQ ID NOS: 37

SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 31
LENGTH: 297
TYPE: PR1
ORGANISM: Homo sapien
US-09-811-094-31

Query Match 89.8%; Score 1385.5; DB 9; Length 297;
Best Local Similarity 87.2%; Pred. No. 5.5e-140;
Matches 260; Conservative 21; Mismatches 16; Indels 1; Gaps 1;

QY 1 MTEOATSFADFLAGGIAAISTKTAAPIERVKLLQOVHASKQIADKQKIVDCIVR 60
DB 1 MGHANSFLKDFLAGAAGAAVSTKTAAPIERVKLLQOVHASKQIASEKQKIIIDCVR 60
QY 61 IPEOGVLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHKQFRYFAGNLSG 120
DB 61 IPEOGVLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHKQFRYFAGNLSG 120
QY 121 GAAGATSLCFVYPLDFARTRLADVCGSGTEREFGIGDCLVKTNSDGRGLYOGFSVS 180
DB 121 GAAGATSLCFVYPLDFARTRLADVGRR-AQREFHGLGDCIIRIKFSKSDGLRGLYOGFNS 179
QY 181 VOGIIIRAAVFGVYDTAKGMLPDPKNTHTVSMIAQVTAAGVVSYPEDTVRRMM 240
DB 180 VOGIIIRAAVFGVYDTAKGMLPDPKNTHTVSMIAQVTAAGVVSYPEDTVRRMM 239
QY 241 QSGRKGADIMYGTGTCWKRIFRDEGKAFKFGKAMSNTVLRMGGAFLVLYDELKRYI 298
DB 240 QSGRKGADIMYGTGTCWKRIRIADDEGAKAFKFGKAMSNTVLRMGGAFLVLYDEIKRYV 297

RESULT 8
US-09-810-644-31

Sequence 31, Application US/09810644
Patent No. US20020012992A1

GENERAL INFORMATION:
APPLICANT: Anderson, Christen M.
APPLICANT: Davis, Robert E.
APPLICANT: Clevenger, William
APPLICANT: Willey, Sandra Eileen
APPLICANT: Willet, Scott W.
APPLICANT: Szabo, Tomas R.
APPLICANT: Ghosh, Soumitra S.
APPLICANT: Moos, Walter H.
APPLICANT: Pei, Yashong
TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE TRANSLATOR (ANT),
FILE REFERENCE: 660088.4203
CURRENT APPLICATION NUMBER: US/09/810.644
NUMBER OF SEQ ID NOS: 37
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 31
LENGTH: 297
TYPE: PR1
ORGANISM: Homo sapien
US-09-810-644-31

Query Match 89.8%; Score 1385.5; DB 9; Length 297;
Best Local Similarity 87.2%; Pred. No. 5.5e-140;
Matches 260; Conservative 21; Mismatches 16; Indels 1; Gaps 1;

QY 1 MTEOATSFADFLAGGIAAISTKTAAPIERVKLLQOVHASKQIADKQKIVDCIVR 60
DB 1 MGHANSFLKDFLAGAAGAAVSTKTAAPIERVKLLQOVHASKQIASEKQKIIIDCVR 60
QY 61 IPEOGVLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHKQFRYFAGNLSG 120
DB 61 IPEOGVLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHKQFRYFAGNLSG 120
QY 121 GAAGATSLCFVYPLDFARTRLADVCGSGTEREFGIGDCLVKTNSDGRGLYOGFSVS 180
DB 121 GAAGATSLCFVYPLDFARTRLADVCGSGTEREFGIGDCLVKTNSDGRGLYOGFSVS 180

DB 121 GAAGATSLCFVYPLDFARTRLADVGRR-AQREFHGLGDCIIRIKFSKSDGLRGLYOGFNS 179
QY 181 VOGIIIRAAVFGVYDTAKGMLPDPKNTHTVSMIAQVTAAGVVSYPEDTVRRMM 240
DB 180 VOGIIIRAAVFGVYDTAKGMLPDPKNTHTVSMIAQVTAAGVVSYPEDTVRRMM 239
QY 241 QSGRKGADIMYGTGTCWKRIFRDEGKAFKFGKAMSNTVLRMGGAFLVLYDELKRYI 298
DB 240 QSGRKGADIMYGTGTCWKRIRIADDEGAKAFKFGKAMSNTVLRMGGAFLVLYDEIKRYV 297

RESULT 9
US-09-185-904A-31

Sequence 31, Application US/09185904A
Patent No. US2002017185A1

GENERAL INFORMATION:
APPLICANT: Anderson, Christen M.
APPLICANT: Davis, Robert E.
APPLICANT: Clevenger, William
APPLICANT: Willey, Sandra Eileen
APPLICANT: Willet, Scott W.
APPLICANT: Szabo, Tomas R.
APPLICANT: Ghosh, Soumitra S.
TITLE OF INVENTION: PRODUCTION OF ADENINE NUCLEOTIDE
TITLE OF INVENTION: TRANSLATOR (ANT), NOVEL ANT LIGANDS AND SCREENING ASSAYS
FILE REFERENCE: 660088.420
CURRENT APPLICATION NUMBER: US/09/185.904A
NUMBER OF SEQ ID NOS: 33
SOFTWARE: FastSeq for Windows Version 3.0
SEQ ID NO 31
LENGTH: 297
TYPE: PR1
ORGANISM: Homo sapien
US-09-185-904A-31

Query Match 89.8%; Score 1385.5; DB 10; Length 297;
Best Local Similarity 87.2%; Pred. No. 5.5e-140;
Matches 260; Conservative 21; Mismatches 16; Indels 1; Gaps 1;

QY 1 MTEOATSFADFLAGGIAAISTKTAAPIERVKLLQOVHASKQIADKQKIVDCIVR 60
DB 1 MGHANSFLKDFLAGAAGAAVSTKTAAPIERVKLLQOVHASKQIASEKQKIIIDCVR 60
QY 61 IPEOGVLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHKQFRYFAGNLSG 120
DB 61 IPEOGVLSFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHKQFRYFAGNLSG 120
QY 121 GAAGATSLCFVYPLDFARTRLADVCGSGTEREFGIGDCLVKTNSDGRGLYOGFSVS 180
DB 121 GAAGATSLCFVYPLDFARTRLADVGRR-AQREFHGLGDCIIRIKFSKSDGLRGLYOGFNS 179
QY 181 VOGIIIRAAVFGVYDTAKGMLPDPKNTHTVSMIAQVTAAGVVSYPEDTVRRMM 240
DB 180 VOGIIIRAAVFGVYDTAKGMLPDPKNTHTVSMIAQVTAAGVVSYPEDTVRRMM 239
QY 241 QSGRKGADIMYGTGTCWKRIFRDEGKAFKFGKAMSNTVLRMGGAFLVLYDELKRYI 298
DB 240 QSGRKGADIMYGTGTCWKRIRIADDEGAKAFKFGKAMSNTVLRMGGAFLVLYDEIKRYV 297

RESULT 10
US-09-801-368-252

Sequence 252, Application US/09801368
Patent No. US20020128250A1

GENERAL INFORMATION:
APPLICANT: Busby, Robert
APPLICANT: Cali, Brian
APPLICANT: Hecht, Peter
APPLICANT: Holtzman, Doug
APPLICANT: Madden, Kevin
APPLICANT: Maxon, Mary

APPLICANT: Moughamer, Todd
APPLICANT: Provart, Nicholas
APPLICANT: Rieke, Darrell
TITLE OF INVENTION: GENES THAT ARE MODULATED BY POSTTRANSCRIPTIONAL GENE SILENCING
FILE REFERENCE: 70030-NP
CURRENT APPLICATION NUMBER: US/10/259,165
CURRENT FILING DATE: 2002-09-26
PRIOR APPLICATION NUMBER: US 60/370,620
PRIOR FILING DATE: 2002-04-04
PRIOR APPLICATION NUMBER: US 60/368,327
PRIOR FILING DATE: 2002-03-27
PRIOR APPLICATION NUMBER: US 60/325,277
PRIOR FILING DATE: 2001-09-26
NUMBER OF SEQ ID NOS: 782
SOFTWARE: Patentlist.pl version 3.0.4 (C) 2001 Syngenta
SEQ ID NO 192
LENGTH: 677
TYPE: PRT
ORGANISM: Oryza sativa
US-10-259-165-192

Query Match 44.5%; Score 686; DB 12; Length 677;

Best Local Similarity 50.3%; Pred. No. 1.4e-64;

Matches 155; Conservative 43; Mismatches 86; Indels 22; Gaps 9;

QY 3 EQAIS-PAKDELAGIAAISKTAIVAPIERYKLLQVQ-HASKQIADKQYKIVDCIYR 60
DB 370 EKGISGFMDPMGVSAAVSKTAAPIERIKILIONDEMIKSGRLSHPKGIADCRGR 429
QY 61 IPKQGVSTFRGLANVIRFPTQALNFAFKDKYKQIFLGGVDKHTQFMRYFAGNLASG 120
DB 430 TINDEGVYALMRGTANYIRFPTQALNFAFKDHFRRMFNFKKDK-DGYMKWFAGNLASG 488
QY 121 GAAGATSLCFYPPDEPARTLAAD-VGKSGTEREPRGIDQIVKTKSDGIRGLY---Q 175
DB 489 GAAGACSLFEFYSLDYARTRLANDAKAKKGGGRFNGLDVYRKTLASDGIAGLIPWIQ 548
QY 176 GFSVSVQGIITYRAYFGVDTAK----GMLPDPKNTIIVSWMIAQTVTAVAGVSYR 230
DB 549 HLPVLVS--LSNRGLYCGMYDSLKPVLVGNLQD---NFLASFLGWTITIGAGLASYP 602
QY 231 FDTYRRRMMQSGRKGADIMTGTVCWRKIFRDEGGKAFKGAWSNVLKRGNGAFVLV 290
DB 603 IDTYRRRMMQSGEA--VKYNSSLDAFKQIVAKGAKSLFKGAGANILRAVAGAVLAG 659
QY 291 YDELKQVI 298
DB 660 YDKLQVVV 667

Search completed: August 28, 2003, 19:45:25
Job time : 20.355 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 28, 2003, 19:35:01 ; Search time 20.6898 Seconds

(without alignments)
1385.139 Million cell updates/sec

Title: US-09-811-132-33

Perfect score: 1543

Sequence: 1 MTEQAISFADFLAGIAA.....LRGMGAFLVLYDELKKVI 298

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283308 seqs, 96168682 residues

Total number of hits satisfying chosen parameters: 283308

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database :
1: pir1.*
2: pir2.*
3: pir3.*
4: pir4.*

Pred. NO. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|-------|-------------|--------|-------|---------------------------|
| 1 | 1543 | 100.0 | 298 | 1 | S03894 ADP,ATP carrier pr |
| 2 | 1512 | 98.0 | 298 | 1 | B43646 ADP,ATP carrier pr |
| 3 | 1454 | 94.2 | 298 | 1 | A29132 ADP,ATP carrier pr |
| 4 | 1424 | 92.3 | 298 | 1 | I60173 adenine nucleotide |
| 5 | 1422 | 92.2 | 298 | 1 | XMBO ADP,ATP carrier pr |
| 6 | 1418 | 91.3 | 298 | 1 | S37210 ADP,ATP carrier pr |
| 7 | 1409 | 91.3 | 298 | 1 | A44778 ADP,ATP carrier pr |
| 8 | 1405 | 91.1 | 298 | 1 | S31814 ADP,ATP carrier pr |
| 9 | 1184 | 76.7 | 301 | 1 | S31935 ADP,ATP carrier pr |
| 10 | 1041 | 67.5 | 313 | 2 | T23207 hypothetical prote |
| 11 | 1039 | 67.3 | 313 | 2 | T23850 hypothetical prote |
| 12 | 1038 | 67.3 | 300 | 2 | T25371 hypothetical prote |
| 13 | 993.5 | 64.4 | 300 | 2 | T15206 hypothetical prote |
| 14 | 978 | 63.4 | 339 | 2 | A41677 ADP,ATP carrier pr |
| 15 | 943 | 61.1 | 301 | 2 | S51132 ADP,ATP carrier pr |
| 16 | 778.5 | 50.5 | 307 | 2 | A36582 ADP,ATP carrier pr |
| 17 | 772 | 50.0 | 308 | 1 | S30259 ADP,ATP carrier pr |
| 18 | 769 | 49.8 | 322 | 2 | T40526 adp,atp translocas |
| 19 | 768 | 49.8 | 386 | 2 | T09709 ADP,ATP carrier pr |
| 20 | 766 | 49.6 | 313 | 1 | XMNC ADP,ATP carrier pr |
| 21 | 764 | 49.5 | 326 | 2 | T25728 hypothetical prote |
| 22 | 762.5 | 49.4 | 305 | 2 | S68154 ADP,ATP carrier pr |
| 23 | 760.5 | 49.3 | 318 | 1 | A31978 ADP,ATP carrier pr |
| 24 | 756.5 | 49.0 | 306 | 2 | T20012 hypothetical prote |
| 25 | 750 | 48.6 | 387 | 2 | S14876 ADP,ATP carrier pr |
| 26 | 748 | 48.5 | 386 | 2 | S21974 ADP,ATP carrier pr |
| 27 | 747 | 48.4 | 306 | 2 | T42011 ADP,ATP carrier pr |
| 28 | 747 | 48.4 | 386 | 2 | S17917 ADP,ATP carrier pr |
| 29 | 744 | 48.2 | 387 | 2 | S16568 ADP,ATP carrier pr |

| | | | | | |
|----|-------|------|-----|---|----------------------------|
| 30 | 743 | 48.2 | 379 | 2 | T04608 ADP,ATP carrier pr |
| 31 | 742.5 | 48.1 | 385 | 1 | S29852 ADP,ATP carrier pr |
| 32 | 742 | 48.1 | 382 | 2 | S33630 ADP,ATP carrier pr |
| 33 | 739.5 | 47.9 | 386 | 2 | S14874 ADP,ATP carrier pr |
| 34 | 737.5 | 47.8 | 309 | 2 | A24849 ADP,ATP carrier pr |
| 35 | 734.5 | 47.6 | 379 | 2 | S21313 ADP,ATP carrier pr |
| 36 | 681.5 | 44.2 | 298 | 2 | T24029 hypothetical prote |
| 37 | 520.5 | 33.7 | 327 | 2 | T51577 ADP,ATP translocas |
| 38 | 383 | 24.8 | 325 | 2 | T04273 ADP,ATP translocas |
| 39 | 381 | 24.7 | 39 | 2 | T01729 mitochondrial prote |
| 40 | 372 | 24.1 | 358 | 2 | T45934 mitochondrial solu |
| 41 | 370.5 | 24.0 | 415 | 2 | T46171 hypothetical prote |
| 42 | 369.5 | 23.9 | 381 | 2 | T51158 hypothetical prote |
| 43 | 368 | 23.8 | 475 | 2 | T50686 peroxisomal Ca-dep |
| 44 | 363 | 23.5 | 348 | 2 | D84798 probable mitochon |
| 45 | 344.5 | 22.3 | 332 | 2 | T47703 Ca-dependent solut |

ALIGNMENTS

RESULT 1

S03894

ADP,ATP carrier protein T3 - human

N:Alternate names: ADP,ATP carrier protein T2 (misidentification); mitochondrial ADP,

C:Species: Homo sapiens (man)

C>Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 17-Mar-2000

C:Accession: S03894; B28116

R:Cozens, A.L.; Runswick, M.J.; Walker, J.E.

J. Mol. Biol. 206, 261-280, 1989

A>Title: DNA sequences of two expressed nuclear genes for human mitochondrial ADP/ATP

A:Reference number: S03893; MUID:89236396; PMID:2541251

A:Accession: S03894

A>Status: not compared with conceptual translation

A:Molecule type: DNA

A:Residues: 1-298 <CO2>

R:Roudisworth, J.; Attardi, G.

Proc. Natl. Acad. Sci. U.S.A. 85, 377-381, 1988

A>Title: Two distinct genes for ADP/ATP translocase are expressed at the mRNA level 1

A:Reference number: A94197; MUID:88124845; PMID:2829183

A:Accession: B28116

A:Molecule type: mRNA

A:Residues: 36-104, 'R', 106, 'A', 109-298 <HO2>

A:Cross-References: GB:J03592; NID:9339722; PIDN:AAA36750.1; PID:9339723

A:Experimental source: liver

A:Genetics:

A:Gene: GDB:ANT3; ANT3Y

A:Cross-References: GDB:125184; OMIM:300151; OMIM:403000

A:Map position: Xp22.32-Xp22.32; Yp11.3-Yp11.3

A>Note: there may be some confusion in the assignment of sequences for GDB:ANT2 and G

C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology

C:Keywords: duplication; homodimer; mitochondrion; transmembrane protein

F:2-268/Product: ADP,ATP carrier protein repeat homology <ACPI>

F:5-98/Domain: ADP,ATP carrier protein repeat homology <ACPI>

F:110-202/Domain: ADP,ATP carrier protein repeat homology <ACPI>

F:207-298/Domain: ADP,ATP carrier protein repeat homology <ACPI>

Query Match 100.0%; Score 1543; DB 1; Length 298;

Best Local Similarity 100.0%; Pred. No. 6e-129;

Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

| | | | |
|----|-----|--|-----|
| QY | 1 | MTEQAISFADFLAGIAAISKTAAPFERKLLIQVHASKQIADKQYGIYDCIYR | 60 |
| DB | 1 | MTEQAISFADFLAGIAAISKTAAPFERKLLIQVHASKQIADKQYGIYDCIYR | 60 |
| QY | 61 | IRKQGVLSFWKGNLANVIRFPQALNFAFDKRYKQIFLGVDKHTQFWRYFAGNLASG | 120 |
| DB | 61 | IRKQGVLSFWKGNLANVIRFPQALNFAFDKRYKQIFLGVDKHTQFWRYFAGNLASG | 120 |
| QY | 121 | GAAGATSCFVYPLDFARTRLAADVGKSTEEFRGLGCIYKTRSDGIRLQYGFSS | 180 |
| DB | 121 | GAAGATSCFVYPLDFARTRLAADVGKSTEEFRGLGCIYKTRSDGIRLQYGFSS | 180 |

QY 181 VGGIIIRAAVFEGVYDTAKGMLDPKNTHTLVSMIAQTATVAVGVSYFEDVRRMM 240
 |||||
 Db 181 VGGIIIRAAVFEGVYDTAKGMLDPKNTHTLVSMIAQTATVAVGVSYFEDVRRMM 240

QY 241 QSGRKADIMYTGTVDCWKRIKIFDEGKAFKFGAMSNTLVGMGAFVLVYDELKRYI 298
 |||||
 Db 241 QSGRKADIMYTGTVDCWKRIKIFDEGKAFKFGAMSNTLVGMGAFVLVYDELKRYI 298

RESULT 2

ADP,ATP carrier protein T2 - bovine
 B43646
 C:Species: Bos primigenius taurus (cattle)
 C>Date: 03-Mar-1993 #sequence_revision 03-Mar-1993 #text_change 20-Aug-1999
 C:Accession: B43646
 R:Powell, S.J.; Medd, S.M.; Runswick, M.J.; Walker, J.E.
 Biochemistry 28, 866-873, 1989
 A>Title: Two bovine genes for mitochondrial ADP/ATP translocase expressed differently in
 A:Reference number: A43646; MUID:89229093; PMID:2540808
 A:Accession: B43646
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-298 <POM>
 A:Cross-references: GB:M24103; NID:9529416; PIDN:AAA30769.1; PID:9529417
 C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology
 C:Keywords: duplication; homodimer; mitochondrion; transmembrane protein
 F:5-99/Domain: ADP,ATP carrier protein repeat homology <ACP1>
 F:110-202/Domain: ADP,ATP carrier protein repeat homology <ACP2>
 F:207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>

Query Match 98.0%; Score 1512; DB 2; Length 298;
 Best Local Similarity 97.7%; Pred. No. 3.3e-126;
 Matches 291; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

QY 1 MPEQATSPKDFLAGGIAAISTKVAPIERVKLLQVHASQIADKQKGIYDCIYR 60
 |||||
 Db 1 MPEQATSPKDFLAGGIAAISTKVAPIERVKLLQVHASQIADKQKGIYDCIYR 60

QY 61 IPEQGVLSFWRGNLANVIRYPTQALNFAFKDKYQIPLGVGDKHTQFWRYFAGNLASG 120
 |||||
 Db 61 IPEQGVLSFWRGNLANVIRYPTQALNFAFKDKYQIPLGVGDKHTQFWRYFAGNLASG 120

QY 121 GAAGATSLCFVYPLDPAKRLADVGKSGFERFGLDGLVYITKSDGRGLYOGFSYS 180
 |||||
 Db 121 GAAGATSLCFVYPLDPAKRLADVGKSGFERFGLDGLVYITKSDGRGLYOGFSYS 180

QY 181 VGGIIIRAAVFEGVYDTAKGMLDPKNTHTLVSMIAQTATVAVGVSYFEDVRRMM 240
 |||||
 Db 181 VGGIIIRAAVFEGVYDTAKGMLDPKNTHTLVSMIAQTATVAVGVSYFEDVRRMM 240

QY 241 QSGRKADIMYTGTVDCWKRIKIFDEGKAFKFGAMSNTLVGMGAFVLVYDELKRYI 298
 |||||
 Db 241 QSGRKADIMYTGTVDCWKRIKIFDEGKAFKFGAMSNTLVGMGAFVLVYDELKRYI 298

RESULT 3

ADP,ATP carrier protein T2 - human
 A29132
 N:Alternate names: mitochondrial ADP,ATP translocase 2
 C:Species: Homo sapiens (man)
 C>Date: 17-Mar-2000 #sequence_revision 17-Mar-2000 #text_change 17-Mar-2000
 C:Accession: A29132; C28116
 R:Battini, R.; Ferrari, S.; Kaczmarek, L.; Calabretta, B.; Chen, S.; Baserga, R.
 J. Biol. Chem. 262, 4355-4359, 1987
 A>Title: Molecular cloning of a cDNA for a human ADP/ATP carrier which is growth-regulat
 A:Reference number: A29132; MUID:87166056; PMID:3031073
 A:Accession: A29132
 A:Molecule type: mRNA
 A:Residues: 1-298 <BAT>
 A:Cross-references: GB:J02683; NID:g179246; PIDN:AAA3579.1; PID:g179247
 R:Shouldersworth, J.; Altardi, G.
 Proc. Natl. Acad. Sci. U.S.A. 85, 377-381, 1988
 A>Title: Two distinct genes for ADP/ATP translocase are expressed at the mRNA level in d

A:Reference number: A94197; MUID:86124845; PMID:2629183
 A:Accession: C28116
 A:Molecule type: mRNA
 A:Residues: 47-65,'G','67-110','L','112-161','G','163-298 <HOU>
 A:Cross-references: GB:J03591; NID:g339720; PIDN:AAA36749.1; PID:g339721
 A:Experimental source: Clone PHAT3
 C:Genetics:
 A:Gene: GDB:ANT2; T3; 2F1
 A:Cross-references: GDB:125190; OMIM:300150
 A:Map position: Xq13-q26
 A>Note: there may be some confusion in the assignment of sequences for GDB:ANT2 and G

C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology
 C:Keywords: duplication; homodimer; mitochondrion; transmembrane protein
 F:5-99/Domain: ADP,ATP carrier protein repeat homology <ACP1>
 F:110-202/Domain: ADP,ATP carrier protein repeat homology <ACP2>
 F:207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>

Query Match 94.2%; Score 1454; DB 1; Length 298;
 Best Local Similarity 92.6%; Pred. No. 4.5e-121;
 Matches 274; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

QY 1 MPEQATSPKDFLAGGIAAISTKVAPIERVKLLQVHASQIADKQKGIYDCIYR 60
 |||||
 Db 1 MPEQATSPKDFLAGGIAAISTKVAPIERVKLLQVHASQIADKQKGIYDCIYR 60

QY 61 IPEQGVLSFWRGNLANVIRYPTQALNFAFKDKYQIPLGVGDKHTQFWRYFAGNLASG 120
 |||||
 Db 61 IPEQGVLSFWRGNLANVIRYPTQALNFAFKDKYQIPLGVGDKHTQFWRYFAGNLASG 120

QY 121 GAAGATSLCFVYPLDPAKRLADVGKSGFERFGLDGLVYITKSDGRGLYOGFSYS 180
 |||||
 Db 121 GAAGATSLCFVYPLDPAKRLADVGKSGFERFGLDGLVYITKSDGRGLYOGFSYS 180

QY 181 VGGIIIRAAVFEGVYDTAKGMLDPKNTHTLVSMIAQTATVAVGVSYFEDVRRMM 240
 |||||
 Db 181 VGGIIIRAAVFEGVYDTAKGMLDPKNTHTLVSMIAQTATVAVGVSYFEDVRRMM 240

QY 241 QSGRKADIMYTGTVDCWKRIKIFDEGKAFKFGAMSNTLVGMGAFVLVYDELKRYI 298
 |||||
 Db 241 QSGRKADIMYTGTVDCWKRIKIFDEGKAFKFGAMSNTLVGMGAFVLVYDELKRYI 298

RESULT 4

adenine nucleotide translocase - rat
 I60173
 C:Species: Rattus norvegicus (Norway rat)
 C>Date: 02-Aug-1996 #sequence_revision 02-Aug-1996 #text_change 20-Aug-1999
 C:Accession: I60173
 R:Shiohara, Y.; Kamada, M.; Yamazaki, N.; Terada, H.
 Blochim. Biophys. Acta 1152, 192-196, 1993
 A>Title: Isolation and characterization of cDNA clones and a genomic clone encoding r
 A:Reference number: I60173; MUID:94002161; PMID:8399300
 A:Accession: I60173
 A>Status: preliminary; translated from GB/EMBL/DBJ
 A:Molecule type: DNA
 A:Residues: 1-298 <RES>
 A:Cross-references: EMBL:X61667; NID:g400426; PIDN:CAA43842.1; PID:g400427
 C:Genetics:
 A:Gene: ant1
 A:Introns: 37/3; 200/1; 247/1
 C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology
 C:Keywords: duplication; homodimer; transmembrane protein
 F:5-99/Domain: ADP,ATP carrier protein repeat homology <ACP1>
 F:110-202/Domain: ADP,ATP carrier protein repeat homology <ACP2>
 F:207-298/Domain: ADP,ATP carrier protein repeat homology <ACP3>

Query Match 92.3%; Score 1424; DB 2; Length 298;
 Best Local Similarity 89.6%; Pred. No. 2e-118;
 Matches 267; Conservative 18; Mismatches 13; Indels 0; Gaps 0;

QY 1 MPEQATSPKDFLAGGIAAISTKVAPIERVKLLQVHASQIADKQKGIYDCIYR 60
 |||||
 Db 1 MPEQATSPKDFLAGGIAAISTKVAPIERVKLLQVHASQIADKQKGIYDCIYR 60

QY 61 IPKEGVLISFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFWRYPAGNLSG 120
 DB 61 IPKEGVLISFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFWRYPAGNLSG 120
 QY 121 GAAGATSLCFEYVPDLPFARTRLAADVKGSGTEREFGLDCLVTKTKSGIRGLYGFVS 180
 DB 121 GAAGATSLCFEYVPDLPFARTRLAADVKGSGTEREFGLDCLVTKTKSGIRGLYGFVS 180
 QY 181 VGGIITVRAAYGVYDPAKGMPLDPKNTHTIVSWMIAGTVAAGVSYPTVRRMM 240
 DB 181 VGGIITVRAAYGVYDPAKGMPLDPKNTHTIVSWMIAGTVAAGVSYPTVRRMM 240
 QY 241 OSGRGADIMYTGTVDCWKRKIFRDEGKAFFKGANSNVLKRGGAFLVLYDELKRV 298
 DB 241 OSGRGADIMYTGTVDCWKRKIFRDEGKAFFKGANSNVLKRGGAFLVLYDELKRV 298

RESULT 5

AMBO
 ADP/ATP carrier protein T1 - bovine
 N:Alternate names: ADP/ATP translocase T1
 C:Species: Bos primigenius taurus (cattle)
 C>Date: 14-Nov-1993 #sequence_revision 22-Jul-1994 #text_change 22-Jun-1999
 C:Accession: A43646; A24822; A03181; A61343; S69369
 R:Powell, S.J.; Medd, S.M.; Rumsack, M.J.; Walker, J.E.
 Biochemistry 28, 866-873, 1989
 A>Title: Two bovine genes for mitochondrial ADP/ATP translocase expressed differently in
 A:Reference number: A43646; MUID:89229093; PMID:2540808
 A:Accession: A43646
 A:Molecule type: mRNA
 A:Residues: 1-298 <POM>
 R:Rasmussen, U.B.; Mohlrad, H.
 Biochem. Biophys. Res. Commun. 138, 850-857, 1986
 A>Title: Bovine cardiac mitochondrial ADP/ATP carrier: two distinct mRNAs and an unusual
 A:Reference number: A24822; MUID:86295775; PMID:3017341
 A:Accession: A24822
 A:Molecule type: mRNA
 A:Residues: 208-298 <RAS>
 A:Cross-references: GB:M13783; NID:9162630; PIDN:AAA30363.1; PID:9162631
 R:Aquila, H.; Mistr, D.; Eulitz, M.; Klingenberg, M.
 Hoppe-Seyler's Z. Physiol. Chem. 369, 345-349, 1982
 A>Title: Complete amino acid sequence of the ADP/ATP carrier from beef heart mitochondrion
 A:Reference number: A03181; MUID:82188267; PMID:7076130
 A:Accession: A03181
 A:Molecule type: protein
 A:Residues: 2-51, 'X', 53-70, 'X', 72-109, 'X', 111-298 <MO>
 A>Note: residue 52 may be methyllysine
 R:Babel, W.; Wachter, E.; Aquila, H.; Klingenberg, M.
 Biochim. Biophys. Acta 670, 176-180, 1981
 A>Title: Amino acid sequence determination of the ADP/ATP carrier from beef heart mitochondrion
 A:Reference number: A61343; MUID:82044680; PMID:6271240
 A:Accession: A61343
 A:Molecule type: protein
 A:Residues: 205-298 <BAB>
 R:Oetmeier, W.; Masson, K.; Kalinna, S.
 Eur. J. Biochem. 227, 730-733, 1995
 A>Title: [(3)H]-azido-4-isopropylaziridine labels Cys159 of the bovine mitochondrial ADP
 A:Reference number: S69369; MUID:95172058; PMID:7867632
 A:Accession: S69369
 A:Molecule type: protein
 A:Residues: 49-63;154-168 <DET>
 C:Comment: This protein is synthesized in the cytosol and transported into the mitochondrion
 C:Complex: homodimer
 C:Function:
 A:Description: catalyzes the exchange between cytosolic ADP and mitochondrial ATP genera
 A>Note: located in the inner mitochondrial membrane
 C:Superfamily: ADP/ATP carrier protein; ADP/ATP carrier protein repeat homology
 C:Keywords: acetylated amino end; duplication; homodimer; methylated amino acid; mtchoch
 F:110-202/Domain: ADP/ATP carrier protein repeat homology <ACP1>
 F:110-202/Domain: ADP/ATP carrier protein repeat homology <ACP2>
 F:207-298/Domain: ADP/ATP carrier protein repeat homology <ACP3>

F:2/Modified site: acetylated amino end (Ser) (in mature form) #status experimental
 F:52/Modified site: N6-methyllysine (Lys) #status predicted

Query Match 92.2%; Score 1422; DB 1; Length 298;
 Best Local Similarity 89.3%; Pred. No. 3,1e-118;
 Matches 265; Conservative 19; Mismatches 13; Indels 0; Gaps 0;

QY 1 MTEQAISPAKDFLAGIAAISTKTAVERKLLIQVHASKQIAADKQYGIYDCYR 60
 DB 1 MSDQALSLKDFLAGIAAISTKTAVERKLLIQVHASKQISAEQYGIYDCYR 60
 QY 61 IPKEGVLISFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFWRYPAGNLSG 120
 DB 61 IPKEGVLISFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFWRYPAGNLSG 120
 QY 121 GAAGATSLCFEYVPDLPFARTRLAADVKGSGTEREFGLDCLVTKTKSGIRGLYGFVS 180
 DB 121 GAAGATSLCFEYVPDLPFARTRLAADVKGSGTEREFGLDCLVTKTKSGIRGLYGFVS 180
 QY 181 VGGIITVRAAYGVYDPAKGMPLDPKNTHTIVSWMIAGTVAAGVSYPTVRRMM 240
 DB 181 VGGIITVRAAYGVYDPAKGMPLDPKNTHTIVSWMIAGTVAAGVSYPTVRRMM 240
 QY 241 OSGRGADIMYTGTVDCWKRKIFRDEGKAFFKGANSNVLKRGGAFLVLYDELKRV 298
 DB 241 OSGRGADIMYTGTVDCWKRKIFRDEGKAFFKGANSNVLKRGGAFLVLYDELKRV 298

RESULT 6

S37210
 ADP/ATP carrier protein T1 - mouse
 N:Alternate names: adenine nucleotide carrier
 C:Species: Mus musculus (house mouse)
 C>Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 20-Aug-1999
 C:Accession: S37210
 R:Laplace, C.; Costec, P.
 submitted to the EMBL Data Library, September 1993
 A:Reference number: S37210
 A:Accession: S37210
 A>Status: preliminary
 A:Molecule type: mRNA
 A:Residues: 1-298 <LAP>
 A:Cross-references: EMBL:X74510; NID:9402627; PIDN:CAA52616.1; PID:9402628
 C:Genetics:
 A:Gene: ANCL
 C:Superfamily: ADP/ATP carrier protein; ADP/ATP carrier protein repeat homology
 C:Keywords: duplication; transmembrane protein
 F:5-99/Domain: ADP/ATP carrier protein repeat homology <ACP1>
 F:110-202/Domain: ADP/ATP carrier protein repeat homology <ACP2>
 F:207-298/Domain: ADP/ATP carrier protein repeat homology <ACP3>

Query Match 91.9%; Score 1418; DB 2; Length 298;
 Best Local Similarity 88.9%; Pred. No. 6,9e-118;
 Matches 265; Conservative 19; Mismatches 14; Indels 0; Gaps 0;

QY 1 MTEQAISPAKDFLAGIAAISTKTAVERKLLIQVHASKQIAADKQYGIYDCYR 60
 DB 1 MDDQALSLKDFLAGIAAISTKTAVERKLLIQVHASKQISAEQYGIYDCYR 60
 QY 61 IPKEGVLISFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFWRYPAGNLSG 120
 DB 61 IPKEGVLISFWRGNLANVIRYPTQALNFAFKDKYKQIFLGVDKHTQFWRYPAGNLSG 120
 QY 121 GAAGATSLCFEYVPDLPFARTRLAADVKGSGTEREFGLDCLVTKTKSGIRGLYGFVS 180
 DB 121 GAAGATSLCFEYVPDLPFARTRLAADVKGSGTEREFGLDCLVTKTKSGIRGLYGFVS 180
 QY 181 VGGIITVRAAYGVYDPAKGMPLDPKNTHTIVSWMIAGTVAAGVSYPTVRRMM 240
 DB 181 VGGIITVRAAYGVYDPAKGMPLDPKNTHTIVSWMIAGTVAAGVSYPTVRRMM 240
 QY 241 OSGRGADIMYTGTVDCWKRKIFRDEGKAFFKGANSNVLKRGGAFLVLYDELKRV 298
 DB 241 OSGRGADIMYTGTVDCWKRKIFRDEGKAFFKGANSNVLKRGGAFLVLYDELKRV 298

F:112-204/Domain: ADP,ATP carrier protein repeat homology <ACP2>
F:209-300/Domain: ADP,ATP carrier protein repeat homology <ACP3>

Query Match 76.7%; Score 1184; DB 1; Length 301;
Best Local Similarity 77.0%; Pred. No. 3, 6e-97;
Matches 231; Conservative 23; Mismatches 44; Indels 2; Gaps 1;

QY 1 MTEQA--ISFAKDLAGGIAAISKTAAPIERVKLLQVQHASQIADQKQKGIYDCI 58
DB 1 MTKKADPYGAFKDLAGGISAASVSTAVAPIERVKLLQVQASQIADQKQKGIYDCI 60
QY 59 VRIPEQGVLSFWKRNLANVIRYPTQALNFAFKQKQKQIPLGVDKTKQFRRYRAGNIA 118
DB 61 VRIPEQGVLSFWKRNLANVIRYPTQALNFAFKQKQKQIPLGVDKTKQFRRYRAGNIA 120
QY 119 SGGAAGATSLCFVYPLDFARTRLAADVGSQTEREFGDGLVTKTSDSIGLYOGFS 178
DB 121 SGGAAGATSLCFVYPLDFARTRLAADVGSQTEREFGDGLVTKTSDSIGLYOGFS 180
QY 179 VSVQGIIRYRAAYFGVYDTAKGMLPDPKNTHTIVSMIAQTVAVAGVSYPEPTVRRRM 238
DB 181 VSVQGIIRYRAAYFGVYDTAKGMLPDPKNTHTIVSMIAQTVAVAGVSYPEPTVRRRM 240
QY 239 MMQSRKADIMYTGTVDCWKRIKIFRDEGKAFKAGMSNVLRGSGAFVLYLYDELKVI 298
DB 241 MMQSRKSEVMYKNTLDCWVKIGKQEGSGAFKAFSNTVLRGSGAFVLYLYDELKVI 300

RESULT 10

T23207

hypothetical protein K01H12.2 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 11-Jan-2000
C:Accession: T23207

R:McMurray, A.

submitted to the EMBL Data Library, December 1995

A:Reference number: 219707

A:Accession: T23207

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-313 <M12>

A:Cross-references: EMBL:268218; PIDN:CAA92472.1; GSPDB:GN00022; CESP:K01H12.2

A:Experimental source: clone K01H12

C:Genetics:

A:Gene: CESP:K01H12.2

A:Map position: 4

A:Introns: 4/1; 191/2

C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology

Query Match 67.5%; Score 1041; DB 2; Length 313;

Best Local Similarity 70.9%; Pred. No. 1, 7e-84;

Matches 207; Conservative 29; Mismatches 52; Indels 4; Gaps 3;

QY 8 FAKDPLAGGIAAISKTAAPIERVKLLQVQHASQIADQKQKGIYDCIYRIPEQGV 67
DB 25 FLIDLASGGTAASVSTAVAPIERVKLLQVQDASITTAADKRYKGIYVLRVPEQGY 84
QY 68 LSFWRGNLANVIRYPTQALNFAFKQKQKQIPLGVDKTKQFRRYRAGNIA 127
DB 85 AALMRGNLANVIRYPTQALNFAFKQKQKQIPLGVDKTKQFRRYRAGNIA 144
QY 128 LCFVYPLDFARTRLAADVGSQTEREFGDGLVTKTSDSIGLYOGFSVSVQGIITY 187
DB 145 LCFVYPLDFARTRLAADVGSQTEREFGDGLVTKTSDSIGLYOGFSVSVQGIITY 203
QY 188 RAAYFGVYDTAKGMLPDPKNTHTIVSMIAQTVAVAGVSYPEPTVRRRM 246
DB 204 RAAYFGVYDTAKGMLPDPKNTHTIVSMIAQTVAVAGVSYPEPTVRRRM 262
QY 247 ADIMYTGTVDCWKRIKIFRDEGKAFKAGMSNVLRGSGAFVLYLYDELKVI 298
DB 263 -DVLKNTLDCAVKTIKNEGMSAMFRGALSNTVLRGSGAFVLYLYDELKVI 313

RESULT 11

T25850

hypothetical protein T01B11.4 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 11-Jan-2000
C:Accession: T25850

R:Geisel, C.; Steilley, L.

submitted to the EMBL Data Library, December 1996

A:Description: The sequence of C. elegans cosmid T01B11.

A:Reference number: 220099

A:Accession: T25850

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-313 <GE1>

A:Cross-references: EMBL:U80931; PIDN:AB38001.1; GSPDB:GN00022; CESP:T01B11.4

A:Experimental source: strain Bristol N2; clone T01B11

C:Genetics:

A:Gene: CESP:T01B11.4

A:Map position: 4

A:Introns: 4/1; 191/2

C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology

Query Match 67.3%; Score 1039; DB 2; Length 313;
Best Local Similarity 70.9%; Pred. No. 2, 6e-84;
Matches 207; Conservative 29; Mismatches 52; Indels 4; Gaps 3;

QY 8 FAKDPLAGGIAAISKTAAPIERVKLLQVQHASQIADQKQKGIYDCIYRIPEQGV 67
DB 25 FLIDLASGGTAASVSTAVAPIERVKLLQVQDASITTAADKRYKGIYVLRVPEQGY 84
QY 68 LSFWRGNLANVIRYPTQALNFAFKQKQKQIPLGVDKTKQFRRYRAGNIA 127
DB 85 AALMRGNLANVIRYPTQALNFAFKQKQKQIPLGVDKTKQFRRYRAGNIA 144
QY 128 LCFVYPLDFARTRLAADVGSQTEREFGDGLVTKTSDSIGLYOGFSVSVQGIITY 187
DB 145 LCFVYPLDFARTRLAADVGSQTEREFGDGLVTKTSDSIGLYOGFSVSVQGIITY 203
QY 188 RAAYFGVYDTAKGMLPDPKNTHTIVSMIAQTVAVAGVSYPEPTVRRRM 246
DB 204 RAAYFGVYDTAKGMLPDPKNTHTIVSMIAQTVAVAGVSYPEPTVRRRM 262
QY 247 ADIMYTGTVDCWKRIKIFRDEGKAFKAGMSNVLRGSGAFVLYLYDELKVI 298
DB 263 -DVLKNTLDCAVKTIKNEGMSAMFRGALSNTVLRGSGAFVLYLYDELKVI 313

RESULT 12

T25371

hypothetical protein T27E9.1 - Caenorhabditis elegans

C:Species: Caenorhabditis elegans
C>Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 11-Jan-2000
C:Accession: T25371

R:Lloyd, C.

submitted to the EMBL Data Library, November 1996

A:Reference number: 220024

A:Accession: T25371

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: DNA

A:Residues: 1-300 <M12>

A:Cross-references: EMBL:282059; PIDN:CAB04874.1; GSPDB:GN00021; CESP:T27E9.1

A:Experimental source: clone T27E9

C:Genetics:

A:Gene: CESP:T27E9.1

A:Map position: 3

A:Introns: 20/1; 41/3; 115/2

C:Superfamily: ADP,ATP carrier protein; ADP,ATP carrier protein repeat homology

Query Match 67.3%; Score 1038; DB 2; Length 300;
Best Local Similarity 69.2%; Pred. No. 3e-84;
Matches 202; Conservative 37; Mismatches 49; Indels 4; Gaps 3;

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: August 28, 2003, 19:28:06 ; Search time 12.0134 Seconds

(without alignments)
1166.524 Million cell updates/sec

Title: US-09-811-132-33

Perfect score: 1543

Sequence: 1 MTEGAISFANDELFLAGIAAA.....LRGNGAFVLVDELKKVI 298

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 127863 seqs, 47026705 residues

Total number of hits satisfying chosen parameters: 127863

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%

Listing first 45 summaries

Database : SwissProt_41:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match length | ID | Description |
|------------|--------|--------------------|------------|---------------------|
| 1 | 1543 | 100.0 | ADP3_HUMAN | P12236 homo sapien |
| 2 | 1512 | 98.0 | ADP3_BOVIN | P32007 bos taurus |
| 3 | 1463 | 94.8 | ADP2_HUMAN | P05141 homo sapien |
| 4 | 1451 | 94.0 | ADP2_RAT | Q09073 rattus norv |
| 5 | 1445 | 93.6 | ADP2_MOUSE | P51881 mus musculu |
| 6 | 1424 | 92.3 | ADP1_RAT | O05962 rattus norv |
| 7 | 1418 | 91.9 | ADP1_MOUSE | P46962 mus musculu |
| 8 | 1417 | 91.8 | ADP1_BOVIN | P02722 bos taurus |
| 9 | 1409 | 91.3 | ADP1_HUMAN | P12235 homo sapien |
| 10 | 1254.5 | 81.3 | ADP1_HUMAN | Q26365 dirosophila |
| 11 | 1204 | 78.0 | ADP1_HUMAN | Q27238 anopheles g |
| 12 | 978 | 65.4 | ADP1_MOUSE | P31692 chlorella k |
| 13 | 778.5 | 50.5 | ADP3_MOUSE | P18238 saccharomyc |
| 14 | 772 | 50.0 | ADP1_MOUSE | P27080 chlamydomon |
| 15 | 769 | 49.8 | ADP1_MOUSE | Q09188 schizosacch |
| 16 | 768 | 49.8 | ADP1_MOUSE | O22342 gossypium h |
| 17 | 766 | 49.6 | ADP1_MOUSE | P02723 neurospora |
| 18 | 762.5 | 49.4 | ADP1_MOUSE | P49382 kluyveromyc |
| 19 | 760.5 | 49.3 | ADP1_MOUSE | P18239 saccharomyc |
| 20 | 750.5 | 48.6 | ADP2_MOUSE | P40941 arabidopsis |
| 21 | 750 | 48.6 | ADP1_MOUSE | P04709 zea mays (m |
| 22 | 748 | 48.5 | ADP1_MOUSE | P25083 solanum tub |
| 23 | 747 | 48.4 | ADP1_MOUSE | P31691 oryza sativ |
| 24 | 744 | 48.2 | ADP2_MOUSE | P12857 zea mays (m |
| 25 | 742.5 | 48.1 | ADP1_MOUSE | P31167 arabidopsis |
| 26 | 740 | 48.0 | ADP1_MOUSE | Q4129 tritricum ae |
| 27 | 739.5 | 47.9 | ADP2_MOUSE | P27081 saccharomyc |
| 28 | 737.5 | 47.8 | ADP1_MOUSE | P04710 saccharomyc |
| 29 | 727 | 47.1 | ADP2_MOUSE | Q41630 tritricum ae |
| 30 | 305.5 | 19.8 | CMC3_MOUSE | O19529 caenorhabdi |
| 31 | 302 | 19.6 | CMC2_MOUSE | O20799 caenorhabdi |
| 32 | 300 | 19.4 | CMC2_MOUSE | O01888 bos taurus |
| 33 | 299 | 19.4 | CMC2_MOUSE | O09297 saccharomyc |

| | | | | | | |
|----|-------|------|-----|---|------------|--------------------|
| 34 | 295 | 19.1 | 678 | 1 | CMC1_HUMAN | O75746 homo sapien |
| 35 | 289.5 | 18.8 | 322 | 1 | GDC_RAT | P16261 rattus norv |
| 36 | 287.5 | 18.6 | 702 | 1 | CMC1_MOUSE | O21153 caenorhabdi |
| 37 | 286 | 18.5 | 325 | 1 | UCP5_HUMAN | O95258 homo sapien |
| 38 | 285 | 18.5 | 332 | 1 | GDC_HUMAN | P16260 homo sapien |
| 39 | 284 | 18.4 | 325 | 1 | UCP5_MOUSE | O92262 mus musculu |
| 40 | 282.5 | 18.3 | 326 | 1 | YE08_SCHPO | O13805 schizosacch |
| 41 | 280 | 18.1 | 675 | 1 | CMC2_HUMAN | O94350 homo sapien |
| 42 | 272 | 17.6 | 315 | 1 | MFT_HUMAN | O912d1 homo sapien |
| 43 | 270 | 17.5 | 315 | 1 | SA18_HUMAN | O911k4 homo sapien |
| 44 | 265 | 17.2 | 312 | 1 | UCP3_HUMAN | P55916 homo sapien |
| 45 | 265 | 17.2 | 676 | 1 | CMC2_MOUSE | O9qxx4 mus musculu |

ALIGNMENTS

RESULT 1
ADP3_HUMAN STANDARD: PRT: 298 AA.
AC P12236; Q96C49;
DT 01-OCT-1989 (Rel. 12, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE ADP/ATP carrier protein, liver isoform T2 (ADP/ATP translocase 3)
DE (Adenine nucleotide translocator 3) (ANT 3).
GN SLC25A6 OR ANT3.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP MEDLINE=89236396; PubMed=2541251;
RX Cozens A.L., Runswick M.J., Walker J.E.;
RT "DNA sequences of two expressed nuclear genes for human mitochondrial
RT ADP/ATP translocase.";
RT J. Mol. Biol. 206:261-280(1989).
RN [2]
RP SEQUENCE FROM N.A.
RA Zhou J., Yu W., Tang H., Mei G., Tsang Y.T.M., Bouck J., Gibbs R.A.,
RA Margolin J.F.;
RT Submitted (JUL-2000) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE FROM N.A.
RC TISSUE=Brain, Cervix, Eye, and Lung;
RX MEDLINE=22388257; PubMed=12477932;
RA Klausner R.D., Feigold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shennan C.M., Schuler G.D.,
RA Hopkins R.F., Zeeberg B., Bueltow K.H., Schaefer C.F., Bhat N.K.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullighy S.J.,
RA Bosak S.A., McEwan P.J., McKernan R.J., Malek J.A., Gunaratne P.H.,
RA Villalobos D.K., Morley K.C., Hale S., Garcia A.M., Gay L.J., Huylk S.W.,
RA Villalobos D.K., Munzy D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield V.S.N., Krzywinski M.J., Skalska U., Smallus D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RP SEQUENCE OF 36-298 FROM N.A.
RC TISSUE=Liver;
RX MEDLINE=86124645; PubMed=2829183;
RA Houdsworth J., Altardi G.;
RT "Two distinct genes for ADP/ATP translocase are expressed at the mRNA

```

RT level in adult human liver.*;
RL Proc. Natl. Acad. Sci. U.S.A. 85:377-381(1988).
CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
CC MITOCHONDRIAL INNER MEMBRANE.
CC -1- SUBUNIT: Homodimer.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC inner membrane.
CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
CC -----
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DR EMBL: J03592; AAA36750.1; -
DR EMBL: AY007135; AAC01988.1; -
DR EMBL: BC007295; AAH07295.1; -
DR EMBL: BC007850; AAH07850.1; -
DR EMBL: BC008737; AAH08737.1; -
DR EMBL: BC008935; AAH08935.1; -
DR EMBL: BC014775; AAH14775.1; -
DR PIR: S03894; S03894.
DR Genew: HGNC:10992; SLC25A6.
DR MIM: 300151; -
DR GO: GO:0005744; C:mitochondrial inner membrane translocase co. .; TAS.
DR GO: GO:0005471; F:ATP/ADP antiporter activity; NMS.
DR GO: GO:0006854; P:ATP/ADP exchange; TAS.
DR InterPro: IPR002067; Mlt_carrier.
DR InterPro: IPR002030; Mlt_uncoupling.
DR InterPro: IPR001993; Mitoch_carrier.
DR Pfam: PF00153; mito_carr; 3.
DR PRINTS: PR00926; MITOCARRIER.
DR PRINTS: PR00784; MTUNCOUPLING.
DR PROSITE: PS00215; MITOCH_CARRIER; 3.
DR MitoChondrion: Inner membrane; Repeat; Transmembrane; Transport;
DR MultiGene family.
FT TRANSMEM 12 29 1 (POTENTIAL).
FT TRANSMEM 73 91 2 (POTENTIAL).
FT TRANSMEM 117 134 3 (POTENTIAL).
FT TRANSMEM 176 195 4 (POTENTIAL).
FT TRANSMEM 214 231 5 (POTENTIAL).
FT TRANSMEM 273 291 6 (POTENTIAL).
FT REPEAT 1 100 1.
FT REPEAT 101 208 2.
FT REPEAT 209 298 3.
FT CONFLICT 105 108 KHTQ -> RHA (in ref. 4).
FT CONFLICT 242 242 S -> F (in ref. 3; AAH14775).
SQ SEQUENCE 298 AA; 32866 MW; 18534E9F0E49672F CRC64;
Query Match 100.0%; Score 1543; DB 1; Length 298;
Best Local Similarity 100.0%; Pred. No. 3.6e-128;
Matches 298; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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QY 241 QSGRKGADIMYTGIVDCMKRIFFDEGKAEFFKGAWSVNLKMGAFVLYVYDELKKYI 298
DB 241 QSGRKGADIMYTGIVDCMKRIFFDEGKAEFFKGAWSVNLKMGAFVLYVYDELKKYI 298
RESULT 2
ADT3_BOVIN STANDARD; PRT; 298 AA.
ID ADT3_BOVIN
AC P32007;
DT 01-JUL-1993 (Rel. 26, Last sequence update)
DT 01-JUL-1993 (Rel. 40, Last annotation update)
DE ADP/ATP carrier protein, isoform T2 (ADP/ATP translocase 3) (Adenine
DE nucleotide translocator 3) (ANT 3).
GN SLC25A6 OR ANT3.
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovidae; Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP MEDLINE=89229093; PubMed=2540808;
RA Powell S.J., Mead S.M., Runswick M.J., Walker J.E.;
RT "Two bovine genes for mitochondrial ADP/ATP translocase expressed
RT differences in various tissues."
RL Biochemistry 28:866-873(1989).
CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
CC MITOCHONDRIAL INNER MEMBRANE.
CC -1- SUBUNIT: Homodimer.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC inner membrane.
CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
CC -----
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CC -----
DR EMBL: M24103; AAA30769.1; -
DR PIR: B43646; B43646.
DR InterPro: IPR002067; Mlt_carrier.
DR InterPro: IPR002030; Mlt_uncoupling.
DR InterPro: IPR001993; Mitoch_carrier.
DR Pfam: PF00153; mito_carr; 3.
DR PRINTS: PR00926; MITOCARRIER.
DR PRINTS: PR00784; MTUNCOUPLING.
DR PROSITE: PS00215; MITOCH_CARRIER; 3.
DR MitoChondrion: Inner membrane; Repeat; Transmembrane; Transport;
DR MultiGene family.
FT TRANSMEM 12 29 1 (POTENTIAL).
FT TRANSMEM 73 91 2 (POTENTIAL).
FT TRANSMEM 117 134 3 (POTENTIAL).
FT TRANSMEM 176 195 4 (POTENTIAL).
FT TRANSMEM 214 231 5 (POTENTIAL).
FT TRANSMEM 273 291 6 (POTENTIAL).
FT REPEAT 2 111 1.
FT REPEAT 112 208 2.
FT REPEAT 209 298 3.
SQ SEQUENCE 298 AA; 32877 MW; 1C34E7DE6E4061 CRC64;
Query Match 98.0%; Score 1512; DB 1; Length 298;
Best Local Similarity 97.7%; Pred. No. 1.9e-125;
Matches 291; Conservative 4; Mismatches 3; Indels 0; Gaps 0;

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OY 61 IPKEGVLSFWKGNLANVIRFPTQALNFAEKDKYKQIFLGVDKHTQFWRYFAQNLASG 120
DB 61 IPKEGVLSFWKGNLANVIRFPTQALNFAEKDKYKQIFLGVDKHTQFWRYFAQNLASG 120
OY 121 GAAGTSLCFYPPDLPARTRLADYKSGTEREFGDCLVTKTSQIRGLYOGFSVS 180
DB 121 GAAGTSLCFYPPDLPARTRLADYKSGTEREFGDCLVTKTSQIRGLYOGFSVS 180
OY 181 VGGIITTYRAAYFGYVDYAKGMLPDPKNTHTIVVSMIAQTVTAAGVSTPPTVRRMM 240
DB 181 VGGIITTYRAAYFGYVDYAKGMLPDPKNTHTIVVSMIAQTVTAAGVSTPPTVRRMM 240
OY 241 QSGRGADIMYTGVDYKWKIRFDEGKAFKFGAMSNVLRGNGAFVLYLDELKVI 298
DB 241 QSGRGADIMYTGVDYKWKIRFDEGKAFKFGAMSNVLRGNGAFVLYLDELKVI 298

RESULT 3
ADT2_HUMAN STANDARD: PRT; 298 AA.
AC P05141; O43350;
DT 13-AUG-1987 (Rel. 05, Created)
DT 01-OCT-1994 (Rel. 30, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE ADP carrier protein, fibroblast isoform (ADP/ATP translocase 2)
DE (Adenine nucleotide translocator 2) (ANT 2).
GN SLC25A5 OR ANT2.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Homiidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE-Placenta;
RX MEDLINE=90375457; PubMed=2168878;
RA Ku D.-H., Kagan J., Chen S.-T., Chang C.-D., Baserga R., Wuzel J.;
RT "The human fibroblast adenine nucleotide translocator gene. Molecular
RT cloning and sequence."
RL J. Biol. Chem. 265:16060-16063(1990).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE=87166056; PubMed=3031073;
RA Battini R., Ferrari S., Kaczmarek L., Calabretta B., Chen S.T.,
RA Baserga R.;
RT "Molecular cloning of a cDNA for a human ADP/ATP carrier which is
RT growth-regulated."
RL J. Biol. Chem. 262:4355-4358(1987).
RN [3]
RP SEQUENCE FROM N.A.
RX Chen C.N., Su Y., Baybayan P., Slijmo A., Nagaraia R.,
RA Mazarelli R.A., Schlesinger D., Chen E.Y.;
RL Submitted (JUN-1996) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A.
RX Becker M., Graves T., Ozersky P.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
RN [5]
RP SEQUENCE OF 47-298 FROM N.A.
RC TISSUE-Liver;
RX MEDLINE=88124645; PubMed=2829183;
RA Houldsworth J., Atford G.;
RT "Two distinct genes for ADP/ATP translocase are expressed at the mRNA
RT level in adult human liver."
RL Proc. Natl. Acad. Sci. U.S.A. 85:377-381(1988).
CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
CC MITOCHONDRIAL INNER MEMBRANE.
CC -1- SUBUNIT: Homodimer.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC inner membrane.
CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
CC -----

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CC -----
DR EMBL; M57424; AAA51737.1; -
DR EMBL; J02683; AAA35579.1; -
DR EMBL; L78810; AAB39266.1; -
DR EMBL; AC004000; AAB96347.1; -
DR EMBL; J03591; AAA6749.1; -
DR PIR; A29132; A29132.
DR Genem; HGNC:10991; SLC25A5.
DR MIM; 300150; -
DR GO; GO:0005887; C: integral to plasma membrane; TAS.
DR GO; GO:0015207; F: adenine transporter activity; TAS.
DR GO; GO:0006832; P: small molecule transport; TAS.
DR InterPro; IPR002067; MLC carrier.
DR InterPro; IPR002030; MLC uncoupling.
DR InterPro; IPR001993; Mitoch. carrier.
DR Pfam; PF00153; mito. carr. 3.
DR PRINTS; PR00926; MITOCARRIER.
DR PRINTS; PR00784; MTUNCOUPLING.
DR PROSITE; PS00215; MITOCH. CARRIER; 3.
KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
KW Multigene family.
FT TRANSMEK 12.. 29
FT TRANSMEK 73.. 91
FT TRANSMEK 117.. 134
FT TRANSMEK 176.. 195
FT TRANSMEK 214.. 231
FT TRANSMEK 273.. 291
FT REPEAT 1.. 111
FT REPEAT 112.. 208
FT REPEAT 209.. 298
FT CONFLICT 6.. 6
FT CONFLICT 66.. 66
FT CONFLICT 111.. 111
FT CONFLICT 162.. 162
SQ SEQUENCE 298 AA; 32895 MW; F973CAED92C49D3 CRC64;

Query Match 94.8%; Score 1463; DB 1; Length 298;
Best Local Similarity 92.9%; Pred. No. 3; 8e-121;
Matches 275; Conservative 13; Mismatches 8; Indels 0; Gaps 0;

OY 1 MTEQAIISPAKDFLAGIAAISKTAIVAPIERVKLLIQVOHASKQITADKQYGIYDCIVR 60
DB 1 MTEQAVSFAPKDFLAGVAIAISKTAIVAPIERVKLLIQVOHASKQITADKQYGIYDCIVR 60
OY 61 IPKEGVLSFWKGNLANVIRFPTQALNFAEKDKYKQIFLGVDKHTQFWRYFAQNLASG 120
DB 61 IPKEGVLSFWKGNLANVIRFPTQALNFAEKDKYKQIFLGVDKHTQFWRYFAQNLASG 120
OY 121 GAAGTSLCFYPPDLPARTRLADYKSGTEREFGDCLVTKTSQIRGLYOGFSVS 180
DB 121 GAAGTSLCFYPPDLPARTRLADYKSGTEREFGDCLVTKTSQIRGLYOGFSVS 180
OY 181 VGGIITTYRAAYFGYVDYAKGMLPDPKNTHTIVVSMIAQTVTAAGVSTPPTVRRMM 240
DB 181 VGGIITTYRAAYFGYVDYAKGMLPDPKNTHTIVVSMIAQTVTAAGVSTPPTVRRMM 240
OY 241 QSGRGADIMYTGVDYKWKIRFDEGKAFKFGAMSNVLRGNGAFVLYLDELKVI 296
DB 241 QSGRGADIMYTGVDYKWKIRFDEGKAFKFGAMSNVLRGNGAFVLYLDELKVI 296

RESULT 4
ADT2_RAT STANDARD: PRT; 298 AA.
AC Q09073;
DT 01-FEB-1995 (Rel. 31, Created)

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DT 01-FEB-1995 (Rel. 31, Last sequence update)
DE 16-OCT-2001 (Rel. 40, Last annotation update)
DE ADP/ATP carrier protein, fibroblast isoform (ADP/ATP translocase 2)
DE (Adenine nucleotide translocator 2) (ANT 2).
GN SLC25A5 OR ANT2.
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
ON NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Liver;
RX MEDLINE=94002161; PubMed=8399300;
RA Shinozaki Y., Kamada M., Yamazaki N., Terada H.;
RT "Isolation and characterization of cDNA clones and a genomic clone
RT encoding rat mitochondrial adenine nucleotide translocator.";
RL Blochum. Biophys. Acta 1152:192-196(1993).
CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
CC MITOCHONDRIAL INNER MEMBRANE.
CC -1- SUBUNIT: Homodimer.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC inner membrane.
CC -1- TISSUE SPECIFICITY: PRESENT IN KIDNEY, BRAIN, HEART, LIVER AND
CC SKELETAL MUSCLE.
CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
CC -----
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CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL: D12771; BAA02338.1; -
DR InterPro: IPR002067; Mit_carrier.
DR InterPro: IPR002030; Mit_uncoupling.
DR InterPro: IPR001993; Mitoch_carrier.
DR Pfam: PF00153; Mitoc_cartr. 3.
DR PRINTS: PR00926; MITOCARTRIER.
DR PRINTS: PR00784; MTUNCOUPLING.
DR PROSITE: PS00215; MITOCH_CARRIER. 3.
KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
KW Multigene family.
FT TRANSMEM 12 29 1 (POTENTIAL).
FT TRANSMEM 73 91 2 (POTENTIAL).
FT TRANSMEM 117 134 3 (POTENTIAL).
FT TRANSMEM 176 195 4 (POTENTIAL).
FT TRANSMEM 214 231 5 (POTENTIAL).
FT TRANSMEM 273 291 6 (POTENTIAL).
FT REPEAT 1 111 1.
FT REPEAT 112 208 2.
FT REPEAT 209 298 3.
SQ SEQUENCE 298 AA; 32901 MW; 6A59204B987EF35 CRC64;
Query Match 94.0%; Score 1451; DB 1; Length 298;
Best Local Similarity 91.9%; Pred. No. 4, 3e-120;
Matches 272; Conservative 15; Mismatches 9; Indels 0; Gaps 0;

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DB 181 VGGIITIRAAVFGVDTAGGMLPDKNTHTVVSMMIAQVTVANAGVSTPFDIVRRMM 240
|||
OY 241 QSGRKGADIMWTCTVDCMKRIFFDEGKAFKFGKANSNVLKMGAGVLYLYDELK 296
|||
DB 241 QSGRKGTIDIMWTCTDCKRIADDEGKAFKFGKANSNVLKMGAGVLYLYDEIK 296
|||
RESULT 5
ADP2_MOUSE STANDARD: PRT: 298 AA.
ID ADP2_MOUSE
AC P51881; O61311; -
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 28-FEB-2003 (Rel. 41, Last annotation update)
DE ADP/ATP carrier protein, fibroblast isoform (ADP/ATP translocase 2)
DE (Adenine nucleotide translocator 2) (ANT 2).
GN SLC25A5 OR ANT2.
OS Mus musculus (Mouse).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
ON NCBI_TaxID=10090;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=C57BL/6; TISSUE=Brain;
RX MEDLINE=97059403; PubMed=8903724;
RA Ellison J.W., Li X., Francke U., Shapiro L.J.;
RT "Rapid evolution of human pseudautosomal genes and their mouse
RT homologs.";
RL Mamm. Genome 7:25-30(1996).
[2]
SEQUENCE FROM N.A.
RC TISSUE=Skeletal muscle;
RA Sheldon J.G.;
RL Thesis (1995), University of Cambridge, U.K.
[3]
SEQUENCE FROM N.A.
RC STRAIN=129/SV;
RA Costel P., Laplace C.;
RL Submitted (FEB-1993) to the EMBL/GenBank/DBJ databases.
[4]
REVIEWS.
RA Laplace C.;
RL Submitted (FEB-1997) to the EMBL/GenBank/DBJ databases.
[5]
SEQUENCE FROM N.A.
RX MEDLINE=20432087; PubMed=10974536;
RA Levy S.E., Chen Y.-S., Graham B.H., Wallace D.C.;
RT "Expression and sequence analysis of the mouse adenine nucleotide
RT translocase 1 and 2 genes.";
RL Gene 254:57-66(2000).
CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
CC MITOCHONDRIAL INNER MEMBRANE.
CC -1- SUBUNIT: Homodimer.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC inner membrane.
CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
CC EMBL: U27316; AAC52838.1; -
CC EMBL: U10404; AAA19009.1; -
CC EMBL: X70847; CAA50196.1; -
CC EMBL: AF240003; AAF64471.1; -
CC MGD: MGI:1353496; SLC25a5.
DR InterPro: IPR002067; Mit_carrier.

```

DR InterPro: IPR002030; Mit_uncoupling.
 DR InterPro: IPR001993; Mitoch_carrier.
 DR Pfam: PF00153; mito_carr; 3.
 DR PRINTS: PRO0926; MITOCARRIER.
 DR PRINTS: PRO0784; MTUNCOUPLING.
 DR PROSITE: PS00215; MITOCH_CARRIER; 3.
 DR Mitochondlion; Inner membrane; Repeat; Transmembrane; Transport;
 KM Multigene family.
 FT TRANSMEM 12 29 1 (POTENTIAL).
 FT TRANSMEM 73 91 2 (POTENTIAL).
 FT TRANSMEM 117 134 3 (POTENTIAL).
 FT TRANSMEM 176 195 4 (POTENTIAL).
 FT TRANSMEM 214 231 5 (POTENTIAL).
 FT TRANSMEM 273 291 6 (POTENTIAL).
 FT REPEAT 1 111 1.
 FT REPEAT 112 208 2.
 FT REPEAT 209 298 3.
 SQ SEQUENCE 298 AA; 32931 MM; 0798E04B987EFE20 CRC64;
 Query Match 93.6%; Score 1445; DB 1; Length 298;
 Best Local Similarity 91.6%; Pred. No. 1.4e-119;
 Matches 271; Conservative 15; Mismatches 10; Indels 0; Gaps 0;

QY 1 MTEQATSPADFLGAGIAAISTAVAPIERVKLLQVQHSKOIAADKOTKGIYDCIVR 60
 DB 1 MTDAAVSPADFLAGVAAIASTAVAPIERVKLLQVQHSKOITADKQYGIIDCYVR 60
 QY 61 IPKQGVLSFWRGNLANVIRFPQALNFAFKDKYKQJFLGVDKHKQFMRYFAGNLASG 120
 DB 61 IPKQGVLSFWRGNLANVIRFPQALNFAFKDKYKQJFLGVDKHKQFMRYFAGNLASG 120
 QY 121 GAAGATSLCFYYPIDFARTRLAADVGKSGTEREFGGLDCLVKTTSKSGINGLYOGFSVS 180
 DB 121 GAAGATSLCFYYPIDFARTRLAADVGKSGTEREFGGLDCLVKTTSKSGINGLYOGFSVS 180
 QY 121 GAAGATSLCFYYPIDFARTRLAADVGKSGTEREFGGLDCLVKTTSKSGINGLYOGFSVS 180
 DB 121 GAAGATSLCFYYPIDFARTRLAADVGKSGTEREFGGLDCLVKTTSKSGINGLYOGFSVS 180
 QY 181 VQGIITRAAFYGYVDYDAKGLPDPKNTHTVSWMIAGTVAAGVSYPPDYARRMM 240
 DB 181 VQGIITRAAFYGYVDYDAKGLPDPKNTHTVSWMIAGTVAAGVSYPPDYARRMM 240
 QY 241 QSGRKGADIMYTGVDCKRIKIFRDEGKAFKFGAMSNVLRMGAFVLYVDELK 296
 DB 241 QSGRKGADIMYTGVDCKRIKIFRDEGKAFKFGAMSNVLRMGAFVLYVDELK 296

RESULT 6
 ADL1_RAT STANDARD; PRT; 298 AA.
 AC 005962;
 DT 01-FEB-1994 (Rel. 28, Created)
 DT 01-FEB-1994 (Rel. 28, Last sequence update)
 DT 16-OCT-2001 (Rel. 40, Last annotation update)
 DE ADP/ATP carrier protein, heart/skeletal muscle isoform T1 (ADP/ATP
 DE translocase 1) (Adenine nucleotide translocator 1) (ANT 1).
 GN SIC25A4 OR ANTI1.
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
 OX NCBI_TaxID=10116;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN: Sprague-Dawley, and Wistar; TISSUE: Heart, and Liver;
 RA MEDLINE=94002161; PubMed=8399300;
 RA Shinohara Y., Kamida M., Yamazaki N., Terrada H.;
 RT "Isolation and characterization of cDNA clones and a genomic clone
 RT encoding rat mitochondrial adenine nucleotide translocator.",
 RL Biochim. Biophys. Acta 1152:192-196(1993).
 CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
 CC MITOCHONDRIAL INNER MEMBRANE.
 CC -1- SUBUNIT: Homodimer.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
 CC inner membrane.
 CC -1- TISSUE SPECIFICITY: IN HEART, SKELETAL MUSCLE AND TO A LESSER
 CC EXTENT, IN BRAIN AND KIDNEY.

CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
 CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
 CC
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 CC or send an email to license@sib-sib.ch).
 CC
 CC EMBL: X61667; CAA43842.1; -
 CC EMBL: D12770; BA00237.1; -
 CC PIR: I60173; I60173.
 DR InterPro: IPR002067; Mit_carrier.
 DR InterPro: IPR002030; Mit_uncoupling.
 DR InterPro: IPR001993; Mitoch_carrier.
 DR Pfam: PF00153; mito_carr; 3.
 DR PRINTS: PRO0926; MITOCARRIER.
 DR PRINTS: PRO0784; MTUNCOUPLING.
 DR PROSITE: PS00215; MITOCH_CARRIER; 3.
 DR Mitochondlion; Inner membrane; Repeat; Transmembrane; Transport;
 KM Multigene family.
 FT TRANSMEM 12 29 1 (POTENTIAL).
 FT TRANSMEM 73 91 2 (POTENTIAL).
 FT TRANSMEM 117 134 3 (POTENTIAL).
 FT TRANSMEM 176 195 4 (POTENTIAL).
 FT TRANSMEM 214 231 5 (POTENTIAL).
 FT TRANSMEM 273 291 6 (POTENTIAL).
 FT REPEAT 1 110 1.
 FT REPEAT 111 208 2.
 FT REPEAT 209 298 3.
 SQ SEQUENCE 298 AA; 32989 MM; 66704FF78C6BC320 CRC64;
 Query Match 92.3%; Score 1424; DB 1; Length 298;
 Best Local Similarity 89.6%; Pred. No. 1e-117;
 Matches 267; Conservative 18; Mismatches 13; Indels 0; Gaps 0;

QY 1 MTEQATSPADFLGAGIAAISTAVAPIERVKLLQVQHSKOIAADKOTKGIYDCIVR 60
 DB 1 MGDQALSLKPLFIAGIAAISTAVAPIERVKLLQVQHSKOISAKOTKGIIDCYVR 60
 QY 61 IPKQGVLSFWRGNLANVIRFPQALNFAFKDKYKQJFLGVDKHKQFMRYFAGNLASG 120
 DB 61 IPKQGVLSFWRGNLANVIRFPQALNFAFKDKYKQJFLGVDKHKQFMRYFAGNLASG 120
 QY 121 GAAGATSLCFYYPIDFARTRLAADVGKSGTEREFGGLDCLVKTTSKSGINGLYOGFSVS 180
 DB 121 GAAGATSLCFYYPIDFARTRLAADVGKSGTEREFGGLDCLVKTTSKSGINGLYOGFSVS 180
 QY 121 GAAGATSLCFYYPIDFARTRLAADVGKSGTEREFGGLDCLVKTTSKSGINGLYOGFSVS 180
 DB 121 GAAGATSLCFYYPIDFARTRLAADVGKSGTEREFGGLDCLVKTTSKSGINGLYOGFSVS 180
 QY 181 VQGIITRAAFYGYVDYDAKGLPDPKNTHTVSWMIAGTVAAGVSYPPDYARRMM 240
 DB 181 VQGIITRAAFYGYVDYDAKGLPDPKNTHTVSWMIAGTVAAGVSYPPDYARRMM 240
 QY 241 QSGRKGADIMYTGVDCKRIKIFRDEGKAFKFGAMSNVLRMGAFVLYVDELK 298
 DB 241 QSGRKGADIMYTGVDCKRIKIFRDEGKAFKFGAMSNVLRMGAFVLYVDELK 298

RESULT 7
 ADL1_MOUSE STANDARD; PRT; 298 AA.
 AC P48962; O62164;
 ID 01-FEB-1996 (Rel. 33, Created)
 DT 01-FEB-1996 (Rel. 33, Last sequence update)
 DT 28-FEB-2003 (Rel. 41, Last annotation update)
 DT 15-SEP-2003 (Rel. 42, Last annotation update)
 DE ADP/ATP carrier protein, heart/skeletal muscle isoform T1 (ADP/ATP
 DE translocase 1) (Adenine nucleotide translocator 1) (ANT 1) (MANC1).
 GN SIC25A4 OR ANTI1 OR ANCI1.
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 OX NCBI_TaxID=10090;

```

RN [1] SEQUENCE FROM N.A.
RP STRAIN-C57BL/6; TISSUE-Brain;
RC MEDLINE-97059403; PubMed-8903724;
RX Ellison J.W., Li X., Francke U., Shapiro L.J.;
RT "Rapid evolution of human pseudautosomal genes and their mouse
RT homologs.";
RL Mamm. Genome 7:25-30(1996).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN-BALB/c; TISSUE-Muscle;
RA Laplace C., Costet P.;
RN Submitted (SEP-1993) to the EMBL/genbank/DBJ databases.
RP [3]
RP SEQUENCE FROM N.A.
RA Levy S.E., Chen Y.-S., Graham B.H., Wallace D.C.;
RT "Expression and sequence analysis of the mouse adenine
RT translocase 1 and 2 genes.";
RN Submitted (MAR-2000) to the EMBL/genbank/DBJ databases.
RP [4]
RP SEQUENCE FROM N.A.
RC TISSUE-Eye;
RX MEDLINE-22388257; PubMed-12477932;
RA Strusberg R.L., Fehlgold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat M.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Stachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Diatchenko M., Soares M.B., Bonaldi M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carinici P., Prange C.,
RA Raha S.S., Locuelli N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Boeck S.A., McEwen P.J., McKernan K.T., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.W., Gay L.J., Hulky S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahy J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.T., Skalske U., Smallus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RT Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
CC MITOCHONDRIAL INNER MEMBRANE.
CC -1- SUBUNIT: Homodimer.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC inner membrane.
CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
CC -----
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CC -----
DR EMBL: U27315; AAC52837.1; -
DR EMBL: X74510; CA552616.1; -
DR EMBL: AF240002; AAF64470.1; -
DR EMBL: BC003791; AAH03791.1; -
DR EMBL: BC026925; AAH26925.1; -
DR PIR: S37210; S37210.
DR MGI: MGI:1353495; SIC254.
DR InterPro: IPR002067; Mit_carrier.
DR InterPro: IPR002030; Mit_uncoupling.
DR InterPro: IPR001993; Mitoch_carrier.
DR Pfam: PF00153; mito_carr; 3.
DR PRINTS: PR00926; MITOCARRIER.
DR PRINTS: PR00784; MTUNCOUPLING.
DR PROSITE: PS00215; MITOCH_CARRIER; 3.

```

| | |
|---|---|
| KM | Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport; |
| KT | Multigene family. |
| FT | TRANSMEM 12 29 1 (POTENTIAL). |
| FT | TRANSMEM 73 91 2 (POTENTIAL). |
| FT | TRANSMEM 117 134 3 (POTENTIAL). |
| FT | TRANSMEM 176 195 4 (POTENTIAL). |
| FT | TRANSMEM 214 231 5 (POTENTIAL). |
| FT | TRANSMEM 273 291 6 (POTENTIAL). |
| FT | REPEAT 1 110 1. |
| FT | REPEAT 111 208 2. |
| FT | REPEAT 209 298 3. |
| FT | CONFLICT 136 136 F -> L (IN REF. 1). |
| SQ | SEQUENCE 298 AA: 32904 MW: 3A849FEABD0981462 CRC64: |
| Query Match 91.9%; Score 1418; DB 1; Length 298; Best Local Similarity 88.9%; Pred. No. 3.4e-117; Matches 265; Conservative 19; Mismatches 14; Indels 0; Gaps | |
| QY | 1 MTQSQAISFANDFLAGGIAAAISTVAAPIERKRLQLQVHASKQTADAKQRYGYDCIVR 60 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : 1 MGQAALSPFKDLFDLAGGIIAAAVSTAAPIERKRLQLQVHASKQTASAEKQYGIIDCVAR 60 |
| DQ | 61 IPKEQGLSVFWRCNLNANVIRYPEPTQALNFPAKDQYKOIPLGVGDHKTOPFRYFAGNLASG 12 P P E Q G L S V F W R C N L N A N V I R Y P E P T Q A L N F P A K D Q Y K O I P L G V G D H K T O P F R Y F A G N L A S G |
| DQ | 61 IPKEQGLSVWRCNRNLNANVIRYPEPTQALNFPAKDQYKOITLGVGDHKQPFMRFAAGNLASG 12 P P E Q G L S V W R C N R N L N A N V I R Y P E P T Q A L N F P A K D Q Y K O I T L G V G D H K Q P F M R F A A G N L A S G |
| QY | 121 GAAGATSLCFVYPPLDEFARTRLAADVGKSCTEREFRGLDCLVIKYKSDGINLYOGFSYS 18 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : 121 GAAGATSLCFVYPPLDEFARTRLAADVGKSSORBEFNGLDCLVIKIFKSDGLKGLYOGFSYS 18 |
| DQ | 121 GAAGATSLCFVYPPLDEFARTRLAADVGKSSORBEFNGLDCLVIKIFKSDGLKGLYOGFSYS 18 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : |
| QY | 181 VGGIITTYRAAYFCVVYTACGMPLDPDKNTHTIVYSMTLAQVTVTAAGVSYSEPTVRRMM 24 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : 181 VGGIITTYRAAYFCVVYTACGMPLDPDNVNIIVYSMTLAQSVTVAGLVSYSEPTVRRMM 24 |
| QY | 241 QGSRKAGADIWTGTVDCKRIKFDEEGCAFFKGAMSNVLRGAGAFVLVYDELKRV 298 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : 241 QGSRKAGADIWTGTVDCKRIKADDEGANAFFGAMSNTVLRGAGAFVLVYDEIKRV 298 |
| DQ | 241 QGSRKAGADIWTGTVDCKRIKADDEGANAFFGAMSNTVLRGAGAFVLVYDEIKRV 298 : : : : : : : : : : : : : : : : : : : : : : : : : : : : : : |
| RESULT 8 ADTL_BOVIN STANDARD; PRT: 297 AA. ID ADTL_BOVIN STANDARD; PRT: 297 AA. | |
| AC | P02722; 21-JUL-1986 (Rel. 01, Created) |
| DT | 01-JUL-1993 (Rel. 26, last sequence update) |
| DT | 16-OCT-2001 (Rel. 40, last annotation update) |
| DE | ADP/ATP carrier protein, heart isoform T1 (ADP/ATP translocase 1) [Adenine nucleotide translocator 1] (ANT 1). SIC25H4 OR ANT1. |
| GN | Bos taurus (Bovine). |
| OS | Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; OC Bovidae; Bovine; Bos. |
| OX | NCBI_TaxID=9913; |
| RN | [1] |
| RP | SEQUENCE FROM N.A. |
| RX | MEDLINE=89229093; PubMed=2540808; Powell S.J., Medd S.M., Runswick M.J., Walker J.E.; "Two bovine genes for mitochondrial ADP/ATP translocase expressed RT differences in various tissues."; Biochemistry 28:866-873(1989). RN [2] RP SEQUENCE. RX MEDLINE=82188267; PubMed=7076130; Agulla H., Mistra D., Eulitz M., Klingenberg M.; "Complete amino acid sequence of the ADP/ATP carrier from beef heart RT mitochondria."; Hoppe-Seyler's Z. Physiol. Chem. 363:345-349(1982). RN [3] RP SEQUENCE OF 207-297 FROM N.A. RX MEDLINE=86295775; PubMed=3017341; Rasmussen U.B., Wohlbard H.; "Bovine cardiac mitochondrial ADP/ATP-carrier: two distinct mRNAs and |


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RT an unusually short 3'-noncoding sequence."
RL Blochem. Biophys. Res. Commun. 138:850-857(1986).
CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE
CC MITOCHONDRIAL INNER MEMBRANE.
CC -1- SUBUNIT: Homodimer.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC inner membrane.
CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
CC -----
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CC -----
DR EMBL: M13783; AAA30363.1; -
DR EMBL: M24102; AAA30768.1; -
DR PIR: A43646; XMO.
DR InterPro: IPR002067; Mlt_carrier.
DR InterPro: IPR002030; Mlt_uncoupling.
DR InterPro: IPR001993; Mitoch_carrier.
DR Pfam: PF00153; mltc_car; 3.
DR PRINTS: PR00926; MITOCARRIER.
DR PROSITE: PS00784; MITOCOUPLING.
DR PROSITE: PS00215; MITOCH_CARRIER; 3.
DR Mitochondrion: Inner membrane. Repeat: Transmembrane; Transport;
DR Multigene family; Methylation.
FT INIT_MET 0
FT MOD_RES 1 1 BLOCKED.
FT MOD_RES 51 51 METHYLATION (POTENTIAL).
FT TRANSMEM 11 28 1 (POTENTIAL).
FT TRANSMEM 72 90 2 (POTENTIAL).
FT TRANSMEM 116 133 3 (POTENTIAL).
FT TRANSMEM 175 194 4 (POTENTIAL).
FT TRANSMEM 213 230 4 (POTENTIAL).
FT TRANSMEM 272 290 6 (POTENTIAL).
FT REPEAT 1 110 1.
FT REPEAT 111 207 2.
FT REPEAT 208 297 3.
SQ SEQUENCE 297 AA: 32836 MW: A582D3C4A40AEB48 CRC64:
Query Match 91.8%; Score 1417; DB 1; Length 297;
Best Local Similarity 89.2%; Pred. No. 4.1e-117;
Matches 265; Conservative 19; Mismatches 13; Indels 0; Gaps 0;

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DT 01-OCT-1989 (Rel. 12, Created)
DT 01-NOV-1990 (Rel. 16, Last sequence update)
DT 15-SEP-2003 (Rel. 42, Last annotation update)
DE ADP/ATP carrier protein, heart/skeletal muscle isoform T1 (ADP/ATP
DE translocase 1) (Adenine nucleotide translocator 1) (ANT 1).
GN SLC25A4 OR ANT1.
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RX MEDLINE-89236396; PubMed-2541251;
RA Cozens A.L., Runswick M.J., Walker J.E.;
RT "DNA sequences of two expressed nuclear genes for human mitochondrial
RT ADP/ATP translocase.";
RL J. Mol. Biol. 206:261-280(1989).
RN [2]
RP SEQUENCE FROM N.A.
RX MEDLINE-89340499; PubMed-2547778;
RA Li K., Warner C.K., Hodge J.A., Minoshima S., Kudoh J.,
RA Fukuyama R., Maekawa M., Shimizu Y., Shintzu N., Wallace D.C.;
RT "A human muscle adenine nucleotide translocator gene has four exons,
RT is located on chromosome 4, and is differentially expressed.";
RL J. Biol. Chem. 264:13998-14004(1989).
RN [3]
RP SEQUENCE FROM N.A.
RX MEDLINE-88041149; PubMed-2823266;
RA Neckelmann N., Li K., Wade R.P., Shuster R., Wallace D.C.;
RT "cDNA sequence of a human skeletal muscle ADP/ATP translocator: lack
RT of a leader peptide, divergence from a fibroblast translocator cDNA,
RT and coevolution with mitochondrial DNA genes.";
RL Proc. Natl. Acad. Sci. U.S.A. 84:7580-7584(1987).
RN [4]
RP SEQUENCE FROM N.A.
RC TISSUE-Eye;
RX MEDLINE-22388257; PubMed-12477932;
RA Strausberg R.L., Fellngold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shemen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Burow K.H., Schefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diachenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Raha S.S., Loguelli N.A., Peters G.J., Abramson R.D., Mullaly S.J.,
RA Bosch S.A., McKernan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Morley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahney J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Skallus D.E.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalls D.E.,
RA Scherch A., Schein J.E., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length
RT human and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [5]
RP SEQUENCE OF 1-37 FROM N.A.
RC TISSUE-Liver;
RX MEDLINE-88124845; PubMed-2829183;
RA Houldsworth J., Altardi G.;
RT "Two distinct genes for ADP/ATP translocase are expressed at the mRNA
RT level in adult human liver.";
RL Proc. Natl. Acad. Sci. U.S.A. 85:377-381(1988).
RN [6]
RP VARIANTS PRO PRO-114 AND MET-289.
RX MEDLINE-20385067; PubMed-10926541;
RA Kaukonen J., Juselius J.K., Tiranli V., Kyttala A., Zeviani M.,
RA Comi G.P., Keranen J., Peltonen L., Suomala J.,
RT "Role of adenine nucleotide translocator 1 in mtDNA maintenance.";
RL Science 289:782-785(2000).
CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE

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CC MITOCHONDRIAL INNER MEMBRANE.
CC -1- SUBUNIT: Homodimer.
CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial
CC inner membrane.
CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
CC -1- DISEASE: Defects in SLC25A4 are a cause of autosomal dominant
CC progressive external ophthalmoplegia with various mitochondrial
CC DNA deletions (PEO). Patients with PEO have mitochondrial
CC myopathy, progressive external ophthalmoplegia, and other
CC abnormalities associated with multiple different deletions of
CC mitochondrial DNA.
CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
CC
CC -----
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CC
CC -----
CC EMBL: J02966; AAA61223.1; -.
CC EMBL: J03593; AAA36751.1; -.
CC EMBL: J04982; AAA51736.1; -.
CC EMBL: BC008664; AA008664.1; -.
CC PIR: A44778; A44778.
CC Genew: HGNC:10990; SLC25M4.
CC MIM: 157640; -.
CC DR GO: 0005887; C: integral to plasma membrane; TAS.
CC DR GO: 0005739; C: mitochondrion; TAS.
CC DR GO: 0015207; F: adenine transporter activity; TAS.
CC DR GO: 0006091; P: energy pathways; TAS.
CC DR GO: 0000002; P: mitochondrial genome maintenance; TAS.
CC DR GO: 0006832; P: small molecule transport; TAS.
CC DR InterPro: IPR002067; Mlt_carrier.
CC DR InterPro: IPR002030; Mlt_uncoupling.
CC DR InterPro: IPR001993; Mitoch_carrier.
CC DR Pfam: PF00153; mltoc_carr; 3.
CC DR PRINTS: PR00926; MITOCARRIER.
CC DR PRINTS: PR00784; MTUNCOUPLING.
CC DR PROSITE: PS00215; MITOCH_CARRIER; 3.
CC DR Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport;
CC K1 Mitogene family; Disease mutation.
CC KW TRANSMEM 12 1 (POTENTIAL).
CC FT TRANSMEM 73 91 2 (POTENTIAL).
CC FT TRANSMEM 117 134 3 (POTENTIAL).
CC FT TRANSMEM 176 195 4 (POTENTIAL).
CC FT TRANSMEM 214 231 5 (POTENTIAL).
CC FT TRANSMEM 273 291 6 (POTENTIAL).
CC FT REPEAT 1 110 1.
CC FT REPEAT 111 208 2.
CC FT REPEAT 209 298 3.
CC FT VARIANT 114 114 A -> P (IN PRO).
CC FT VARIANT 289 289 V -> M (IN PRO).
CC FT VARIANT 16 16 G -> A (IN REF. 3).
CC FT CONFLICT 147 149 GCA -> RR (IN REF. 3).
CC FT CONFLICT 227 227 V -> L (IN REF. 3).
CC SQ SEQUENCE 298 AA; 33064 MW; 59F0DFAC4E7CBB CRC64;

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Query Match 91.3%; Score 1409; DB 1; Length 298;
Best Local Similarity 88.3%; Pred. No. 2, 1e-116;
Matches 263; Conservative 19; Mismatches 16; Indels 0; Gaps 0;

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QY 1 MTEQALSPKDFLAGLIIAISTAVAPRIKRVLLQVHASQIADKQYKQIVDCYR 60
DB 1 MGHANSEFLKDFLAGVAAVSTAVAPRIKRVLLQVHASQIASEKQYKQIVDCYR 60
QY 61 IPKEQGLTFWFRGNLANVIRYPTQALNFAFKDKYKQIFGVDKHKQFWRVAGNLAG 120
DB 61 IPKEQGLTFWFRGNLANVIRYPTQALNFAFKDKYKQIFGVDKHKQFWRVAGNLAG 120

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QY 121 GAAGATSLCEVYPLDFARTRIAADVCKSGTEREFGIDLVKTRKSDGIRGLYOGFSYS 180
DB 121 GAAGATSLCEVYPLDFARTRIAADVCKSGTEREFGIDLVKTRKSDGIRGLYOGFSYS 180
QY 181 VCGIIIRAAVFGVYDTAKMLDPKNTHTVSGMIAQVYAVAGVSYPTVTRRRMM 240
DB 181 VCGIIIRAAVFGVYDTAKMLDPKNTHTVSGMIAQVYAVAGVSYPTVTRRRMM 240
QY 241 QSGRKGADIMYTGVCQWRKIFPDEGKAFKGMWSVVLKMGAFVLVYDELRKYI 298
DB 241 QSGRKGADIMYTGVCQWRKIFPDEGKAFKGMWSVVLKMGAFVLVYDELRKYI 298

RESULT 10
ID ADT_DROME STANDARD; PRT: 299 AA.
AC Q26365; P91614; Q26254; Q95830; Q9VZ70;
DT 15-JUL-1998 (Rel. 36, Created)
DT 28-FEB-2003 (Rel. 42, Last sequence update)
DE 15-SEP-2003 (Rel. 42, Last annotation update)
DE ADP carrier protein (ADP/ATP translocase) (Adenine nucleotide
DE translocator) (ANT) (Stress sensitive B protein).
GN SSB OR A/A-T OR CGI8944.
OS Drosophila melanogaster (fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7227;
RN [1]
RX MEDLINE=92389367; Pubmed=1387687;
RA Louvi A., Tsiftoglou S.G.;
RT "A cDNA clone encoding the ADP/ATP translocase of Drosophila
RT melanogaster shows a high degree of similarity with the mammalian
RT ADP/ATP translocases."
RJ J. Mol. Evol. 35:44-50(1992).
RN [2]
RX MEDLINE=9435065; Pubmed=7520869;
RA Hutter P., Karch F.;
RT "Molecular analysis of a candidate gene for the reproductive
RT isolation between sibling species of Drosophila."
RJ Experimentalia 50:749-762(1994).
RN [3]
RX MEDLINE=9435065; Pubmed=7520869;
RA Zhang Y.Q., Davis A.W., Roote J., Herrmann S., Ashburner M.;
RT Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
RN [4]
RX MEDLINE=20196006; Pubmed=10731132;
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
RA George R.A., Lewis S., Richards S., Ashburner M., Henderson S.N.,
RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Brandon R.C., Rogers J.H., Blazer R.G., Champe M., Pfeiffer B.D.,
RA Man K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Miklos G.L.G.,
RA April J.F., Aghayani A., An H.-J., Andrews-Pfannkoch C., Baldwin D.,
RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
RA Beeson K.Y., Benos P.V., Berman J.P., Bhandari D., Bolshakov S.,
RA Borokova D., Botchan M.R., Bouck J., Brockstein P., Brotler P.,
RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
RA Dodson R., Doup L.E., Downes M., Dugan-Rocha S., Dunn P.,
RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
RA Folsch C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
RA Hostin D., Houston K.A., Howland T.J., Wei M.-H., Idegawa C.,
RA Jaitai M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,

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FT TRANSMEM 178 197 4 (POTENTIAL).
 FT TRANSMEM 216 233 5 (POTENTIAL).
 FT TRANSMEM 275 293 6 (POTENTIAL).
 SQ SEQUENCE 301 AA; 32863 MW; 4CC9EL7C9F8DA08B CRC64;

Query Match 78.0%; Score 1204; DB 1; Length 301;
 Best Local Similarity 77.7%; Pred. No. 2,1e-98;
 Matches 233; Conservative 23; Mismatches 42; Indels 2; Gaps 1;

QY 1 MTEQA--ISPAKDELACGIAAIAIKTAAPIERVKLLQVOHASKQIADKQYGIYDCI 58
 1 MTKADADYGRKADPLAGISASVKTAVPIERKLLQVOHASKQIADKQYGIYDCI 60

DB 119 SGGAGATSLCFVYPLDFAFRTLRADYKSGTEREFGDCLVTKIRKSGIRGLYGF 178
 121 SGGAGATSLCFVYPLDFAFRTLRADYKSGTEREFGDCLVTKIRKSGIRGLYGF 180

QY 179 VSVGGITTYRAAYFGVYDTAKGMLPDPKNTIIVSMIAQVTVAAGVSYEPDVARRM 238
 181 VSVGGITTYRAAYFGVYDTAKGMLPDPKNTIIVSMIAQVTVAAGVSYEPDVARRM 240

DB 239 MMSGKRGADIMTGYVDCRKRTFRDEGKAFKFGANSNVLKRGAFVLVDELKVI 298
 241 MMSGKRGADIMTGYVDCRKRTFRDEGKAFKFGANSNVLKRGAFVLVDELKVI 300

RESULT 12
 ADT_CHLKE STANDARD; PRT; 339 AA.

AC P31692;
 DT 01-JUL-1993 (Rel. 26, Created)
 DT 01-JUL-1993 (Rel. 26, Last sequence update)
 DT 15-JUL-1998 (Rel. 36, Last annotation update)
 DE ADP,ATP carrier protein (ADP/ATP translocase) (Adenine nucleotide translocator) (ANT).
 OS Chlorocella kessleri.
 OS Eukaryota; Viridiplantae; Chlorophyta; Trebouxiophyceae; Chlorocellales; Chlorocellaceae; Chlorocella.
 CC NCBI_Taxid=3074;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=92084708; Pubmed=1748677;
 RA Hlgarth C., Sauer N., Tanner W.;
 RT "Glucose increases the expression of the ATP/ADP translocator and the glyceroldehyde-3-phosphate dehydrogenase genes in Chlorocella";
 RL J. Biol. Chem. 266:24044-24047(1991).
 CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE MITOCHONDRIAL INNER MEMBRANE.
 CC -1- SUBUNIT: Homodimer (By similarity).
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial inner membrane.
 CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
 CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
 CC
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 CC
 CC EMBL: M76669; AAA33027.1;
 DR PIR: A41677; A41677.
 DR InterPro: IPR002067; Mt_carrier.
 DR InterPro: IPR001993; Mitoch_carrier.
 DR Pfam: PF00153; mito_carr; 3.
 DR PRINTS: PR00926; MITOCARRIER.
 DR PROSITE: PS00215; MITOCH_CARRIER; 3.

KW Mitochondrion; Inner membrane; Repeat; Transmembrane; Transport.
 FT TRANSMEM 45 62 1 (POTENTIAL).
 FT TRANSMEM 108 126 2 (POTENTIAL).
 FT TRANSMEM 151 168 3 (POTENTIAL).
 FT TRANSMEM 209 228 4 (POTENTIAL).
 FT TRANSMEM 248 265 5 (POTENTIAL).
 FT TRANSMEM 304 322 6 (POTENTIAL).
 SQ SEQUENCE 339 AA; 36686 MW; 54779734A33B3942 CRC64;

Query Match 63.4%; Score 978; DB 1; Length 339;
 Best Local Similarity 66.9%; Pred. No. 1.6e-78;
 Matches 198; Conservative 26; Mismatches 64; Indels 8; Gaps 5;

QY 6 ISPAKDELACGIAAIAIKTAAPIERVKLLQVOHASKQIADK--QYKIVDCIYRIPK 63
 39 MAFYKDLADLAGTAGAISKTAAPIERVKLLQVOHASKQIADK--QYKIVDCIYRIPK 98

DB 64 ECGLSFWKRNLANVITFFPQALNFKFKKQKQIFLGVDKHTQFWRITAGNLASGGA 123
 99 ECGLSFWKRNLANVITFFPQALNFKFKKQKQIFLGVDKHTQFWRITAGNLASGGA 157

QY 124 GATSLCFVYPLDFAFRTLRADYKSGTEREFGDCLVTKIRKSGIRGLYGFVSVOG 183
 158 GATSLCFVYPLDFAFRTLRADYKSGTEREFGDCLVTKIRKSGIRGLYGFVSVOG 216

DB 184 IIVRYAAYFGVYDTAKGMLPDPKNTIIVSMIAQVTVAAGVSYEPDVARRMMS 242
 217 IIVRYAAYFGVYDTAKGMLPDPKNTIIVSMIAQVTVAAGVSYEPDVARRMMS 276

QY 243 GKKGADIMTGYVDCRKRTFRDEGKAFKFGANSNVLKRGAFVLVDELKVI 298
 277 GKKGADIMTGYVDCRKRTFRDEGKAFKFGANSNVLKRGAFVLVDELKVI 329

RESULT 13
 ADT3_YEAST STANDARD; PRT; 307 AA.

AC P18238;
 DT 01-NOV-1990 (Rel. 16, Created)
 DT 01-NOV-1990 (Rel. 16, Last sequence update)
 DT 01-OCT-1994 (Rel. 30, Last annotation update)
 DE ADP,ATP carrier protein 3 (ADP/ATP translocase 3) (Adenine nucleotide translocator 3) (ANT 3).
 GN AAC3 OR YBR083W OR YBR0753.
 OS Saccharomyces cerevisiae (Baker's yeast).
 OS Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes; Saccharomycetales; Saccharomycetaceae; Saccharomycetes.
 CC NCBI_Taxid=4932;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=90324269; Pubmed=2165073;
 RA Kolarov J., Kolarova N., Nelson N.;
 RT "A third ADP/ATP translocator gene in yeast";
 RL J. Biol. Chem. 265:12711-12716(1990).
 CC -1- FUNCTION: CATALYZES THE EXCHANGE OF ADP AND ATP ACROSS THE MITOCHONDRIAL INNER MEMBRANE.
 CC -1- SUBUNIT: Homodimer.
 CC -1- SUBCELLULAR LOCATION: Integral membrane protein. Mitochondrial inner membrane.
 CC -1- DOMAIN: COMPOSED OF THREE HOMOLOGOUS DOMAINS.
 CC -1- SIMILARITY: Belongs to the mitochondrial carrier family.
 CC

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OK protein - protein search, using sw model

Run on: August 28, 2003, 19:34:36 ; Search time 50.3897 Seconds
(without alignments)
1526.099 Million cell updates/sec

Title: US-09-811-132-33

Perfect score: 1543
Sequence: 1 MTEQALSFADFLAGLIAA.....LRGKGAFVLVYDELKKVI 298

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 830525 seqs, 258052604 residues

Total number of hits satisfying chosen parameters: 830525

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%
Listing first 45 summaries

Database :

1: SP_ARCHAEA:*
2: SP_BACTERIA:*
3: SP_FUNGI:*
4: SP_HUMAN:*
5: SP_INVERTEBRATE:*
6: SP_MAMMAL:*
7: SP_MNC:*
8: SP_ORGANELLAE:*
9: SP_PHAGE:*
10: SP_PLANT:*
11: SP RODENT:*
12: SP_VIRUS:*
13: SP_VERTEBRATE:*
14: SP_UNCLASSIFIED:*
15: SP_VIRUS:*
16: SP_BACTERIAP:*
17: SP_ARCHAEP:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

| Result No. | Score | Query Match | Length | DB ID | Description |
|------------|--------|-------------|--------|-------|-------------|
| 1 | 1474 | 95.5 | 298 | 13 | OBAYM3 |
| 2 | 1451 | 94.0 | 298 | 6 | OB8QH5 |
| 3 | 1446 | 93.7 | 298 | 13 | OB8QH5 |
| 4 | 1422 | 92.2 | 298 | 6 | OB8QH5 |
| 5 | 1421 | 92.1 | 298 | 13 | OB8QH5 |
| 6 | 1414 | 91.6 | 298 | 11 | OB8QH5 |
| 7 | 1409 | 91.3 | 298 | 13 | OB8QH5 |
| 8 | 1406 | 91.1 | 298 | 13 | OB8QH5 |
| 9 | 1402 | 90.9 | 298 | 13 | OB8QH5 |
| 10 | 1300 | 88.3 | 299 | 5 | O95VX4 |
| 11 | 1259 | 81.6 | 317 | 13 | O91336 |
| 12 | 1254.5 | 81.3 | 312 | 5 | O8IRAO |
| 13 | 1235.5 | 80.1 | 300 | 5 | O9NHWS |
| 14 | 1187.5 | 76.7 | 288 | 5 | O44093 |
| 15 | 1183.5 | 76.7 | 288 | 5 | O44094 |
| 16 | 1176.5 | 76.2 | 304 | 5 | O25129 |

| | | | | | | |
|----|--------|------|-----|----|--------|--------------------|
| 17 | 1159 | 75.1 | 254 | 11 | OB8KQ5 | QB8K9 mus musculus |
| 18 | 1137.5 | 73.7 | 307 | 5 | O62526 | O62526 drosophila |
| 19 | 1119 | 72.5 | 315 | 4 | O9HOC2 | O9HOC2 homo sapien |
| 20 | 1041 | 67.5 | 313 | 5 | O21103 | O21103 caenorhabd |
| 21 | 1039 | 67.3 | 313 | 5 | P91410 | P91410 caenorhabd |
| 22 | 1038 | 67.3 | 300 | 5 | O45865 | O45865 caenorhabd |
| 23 | 1036.5 | 67.2 | 310 | 10 | O8H727 | O8H727 phytothor |
| 24 | 996 | 64.5 | 309 | 5 | O97470 | O97470 dictyostel |
| 25 | 993.5 | 64.4 | 300 | 5 | O01813 | O01813 caenorhabd |
| 26 | 993 | 64.4 | 300 | 5 | O17407 | O17407 caenorhabd |
| 27 | 973.5 | 63.1 | 318 | 5 | O9HJ36 | O9HJ36 toxoplasma |
| 28 | 947 | 61.4 | 301 | 5 | O8J734 | O8J734 plasmodium |
| 29 | 946.5 | 61.3 | 307 | 8 | O9XM22 | O9XM22 ascaris suu |
| 30 | 944 | 61.2 | 301 | 5 | O25692 | O25692 plasmodium |
| 31 | 944 | 61.2 | 301 | 5 | O8WVR4 | O8WVR4 euplores sp |
| 32 | 943 | 61.1 | 301 | 5 | O26006 | O26006 plasmodium |
| 33 | 936 | 60.7 | 305 | 5 | O8WVR7 | O8WVR7 nyctotherus |
| 34 | 932 | 60.4 | 308 | 5 | O8WVR8 | O8WVR8 nyctotherus |
| 35 | 924 | 59.9 | 308 | 5 | O8WVR5 | O8WVR5 nyctotherus |
| 36 | 924 | 59.9 | 308 | 5 | O8WVR6 | O8WVR6 nyctotherus |
| 37 | 827 | 53.6 | 170 | 6 | O9XS69 | O9XS69 sus scrofa |
| 38 | 778.5 | 50.5 | 305 | 3 | O8JOM2 | O8JOM2 yarrowia |
| 39 | 767.5 | 49.7 | 302 | 3 | O8JOM2 | O8JOM2 yarrowia |
| 40 | 764 | 49.5 | 326 | 5 | P91270 | P91270 caenorhabd |
| 41 | 760 | 49.3 | 307 | 5 | O76286 | O76286 trypanosoma |
| 42 | 759 | 49.2 | 303 | 5 | O74260 | O74260 candida par |
| 43 | 756.5 | 48.0 | 306 | 5 | O18683 | O18683 caenorhabd |
| 44 | 753 | 48.8 | 307 | 5 | O26697 | O26697 trypanosoma |
| 45 | 749 | 48.5 | 315 | 3 | O8J0U1 | O8J0U1 gaemannomy |

ALIGNMENTS

RESULT 1
ID OBAYM3 PRELIMINARY; PRT; 298 AA.
AC OBAYM3;
DT 01-MAR-2003 (TREMBLrel. 23, Created)
DT 01-MAR-2003 (TREMBLrel. 23, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE ATP/ADP antiporter.
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RA Toyomizu M., Ueda M., Sato S., Seki Y., Sato K., Akiba Y.;
RT "Cold-induced mitochondrial uncoupling and expression of chicken UCP
and ANT mRNA in chicken skeletal muscle.";
RL FEBS Lett. 0:0-0(2002).
DR EMBL; AB088686; BAC15533.1; -
SQ SEQUENCE 298 AA; 32847 MW; 1174C5E400A10D CRC64;

Query Match 95.5%; Score 1474; DB 13; Length 298;
Best Local Similarity 93.0%; Pred. No. 2.5e-125;
Matches 277; Conservative 14; Mismatches 7; Indels 0; Gaps 0;
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1 MADQALSFADFLAGLIAAISKTAAPIERVKLLLOVHASKQIADKQYGIYDCIYR 60
DB 1 MADQALSFADFLAGLIAAISKTAAPIERVKLLLOVHASKQIADKQYGIYDCIYR 60
OY 61 IRKEQVLSFWRGNTANVIRFPTQALNFAFDKTKQIFLAGVDKHTQFRRFAGNLAGS 120
1 IRKEQVLSFWRGNTANVIRFPTQALNFAFDKTKQIFLAGVDKHTQFRRFAGNLAGS 120
DB 61 IRKEQVLSFWRGNTANVIRFPTQALNFAFDKTKQIFLAGVDKHTQFRRFAGNLAGS 120
OY 121 GAAGATSLCFVYPLDFARTRLAADVGKSTEEFEGKGLGCLYKTRSDGIRGLYGFVS 180
121 GAAGATSLCFVYPLDFARTRLAADVGKSTEEFEGKGLGCLYKTRSDGIRGLYGFVS 180
DB 121 GAAGATSLCFVYPLDFARTRLAADVGKADREDFSGIDCLVTKIKSDRLRGLYGFVS 180

QY 181 VGGIITIRAAVFCGYDTAGKMLPDPKNTHTIVSWMTAQVTAAGVSPEDTVRRMM 240
 DB 181 VGGIITIRAAVFCGYDTAGKMLPDPKNTHTIVSWMTAQVTAAGVSPEDTVRRMM 240
 QY 241 QSGRKADIMYTGTVCMRKIFPDEGKAFKFGKAMSNVLRGMGAFVLYLDELKRYI 298
 DB 241 QSGRKADIMYTGTVCMRKIFPDEGKAFKFGKAMSNVLRGMGAFVLYLDELKRYI 298
 RESULT 2
 OSQSH5 PRELIMINARY; PRT; 298 AA.
 AC OSQSH5;
 DT 01-JUN-2002 (Tremblrel. 21, Created)
 DT 01-JUN-2002 (Tremblrel. 21, Last sequence update)
 DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
 DE Adenine nucleotide translocator 2.
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovidae; Bovinae; Bos.
 NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Yamazaki N., Shinohara Y., Tanida K., Terada H.;
 RT "Structural properties of mammalian mitochondrial ADP/ATP carriers:
 RT Identification of possible amino acids that determine functional
 RT differences in its isoforms";
 RL Mitochondrion 1:371-379(2002).
 DR EMBL; AB065433; BAB84673.1; -;
 DR Interpro: IPR001993; Mitoch_carrier.
 DR Pfam: PF00153; mito_carri; 3.
 DR PROSITE: PS00215; MITOCH_CARRIER; 3.
 SQ SEQUENCE 298 AA; 32955 MW; CB6897BB987B79C0 CRC64;
 Query Match 94.0%; Score 1451; DB 6; Length 298;
 Best Local Similarity 92.2%; Pred. No. 3e-123;
 Matches 273; Conservative 13; Mismatches 10; Indels 0; Gaps 0;
 QY 1 MTEQAISFANDFLAGGIAAISKTAAPIERVKLLQVGHASKQIADKQKGYDCIVR 60
 DB 1 MTEQAISFANDFLAGGIAAISKTAAPIERVKLLQVGHASKQIADKQKGYDCIVR 60
 QY 1 MTEQAISFANDFLAGGIAAISKTAAPIERVKLLQVGHASKQIADKQKGYDCIVR 60
 DB 1 MTEQAISFANDFLAGGIAAISKTAAPIERVKLLQVGHASKQIADKQKGYDCIVR 60
 QY 61 IPREGVLSFWKRNLANVIRYPTQALNFAFKYKQIFLGVDKTKQFWRRFAGNLASG 120
 DB 61 IPREGVLSFWKRNLANVIRYPTQALNFAFKYKQIFLGVDKTKQFWRRFAGNLASG 120
 QY 121 GAAGATSLCFVYPLDPAFRTLRADVGKSGTREFRGIGDCLVTKITSDGIRGLYQGFNS 180
 DB 121 GAAGATSLCFVYPLDPAFRTLRADVGKSGTREFRGIGDCLVTKITSDGIRGLYQGFNS 180
 QY 181 VGGIITIRAAVFCGYDTAGKMLPDPKNTHTIVSWMTAQVTAAGVSPEDTVRRMM 240
 DB 181 VGGIITIRAAVFCGYDTAGKMLPDPKNTHTIVSWMTAQVTAAGVSPEDTVRRMM 240
 QY 241 QSGRKADIMYTGTVCMRKIFPDEGKAFKFGKAMSNVLRGMGAFVLYLDELKRYI 298
 DB 241 QSGRKADIMYTGTVCMRKIFPDEGKAFKFGKAMSNVLRGMGAFVLYLDELKRYI 298
 RESULT 3
 OSQSH5 PRELIMINARY; PRT; 298 AA.
 AC OSQSH5;
 DT 01-OCT-2002 (Tremblrel. 22, Created)
 DT 01-OCT-2002 (Tremblrel. 22, Last sequence update)
 DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
 DE Solute carrier family 25 member 5 protein.
 OS SLC25A5.
 OC Brachydanio rerio (Zebrafish) (Danio rerio).
 OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;
 OC Cyprinidae; Danio.

OX NCBI_TaxID=7955;
 RN [1]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22035902; PubMed=12006978;
 RA Gollig G., Amsterdam A., Sun Z., Antonelli M., Maldonado E., Chen W.,
 RA Burgess S., Haidt M., Artzt K., Farrington S., Lin S.-T., Nissen R.M.,
 RA Hopkins N.;
 RT "Insertional mutagenesis in zebrafish rapidly identifies genes
 RT essential for early vertebrate development.";
 RL Nat. Genet. 31:135-140(2002).
 DR EMBL; AF506216; AAM34660.1; -;
 DR Interpro: IPR001993; Mitoch_carrier.
 DR Interpro: IPR002067; Mit_carrier.
 DR Interpro: IPR002030; Mit_uncoupling.
 DR Pfam: PF00153; mito_carri; 3.
 DR PRINTS: PR00926; MITOCARRIER.
 DR PRINTS: PR00784; MTUNCOUPLING.
 DR PROSITE: PS00215; MITOCH_CARRIER; 3.
 SQ SEQUENCE 298 AA; 32763 MW; D78663CF65C5D39 CRC64;
 Query Match 93.7%; Score 1446; DB 13; Length 298;
 Best Local Similarity 91.9%; Pred. No. 8.5e-123;
 Matches 274; Conservative 15; Mismatches 9; Indels 0; Gaps 0;
 QY 1 MTEQAISFANDFLAGGIAAISKTAAPIERVKLLQVGHASKQIADKQKGYDCIVR 60
 DB 1 MTEQAISFANDFLAGGIAAISKTAAPIERVKLLQVGHASKQIADKQKGYDCIVR 60
 QY 61 IPREGVLSFWKRNLANVIRYPTQALNFAFKYKQIFLGVDKTKQFWRRFAGNLASG 120
 DB 61 IPREGVLSFWKRNLANVIRYPTQALNFAFKYKQIFLGVDKTKQFWRRFAGNLASG 120
 QY 121 GAAGATSLCFVYPLDPAFRTLRADVGKSGTREFRGIGDCLVTKITSDGIRGLYQGFNS 180
 DB 121 GAAGATSLCFVYPLDPAFRTLRADVGKSGTREFRGIGDCLVTKITSDGIRGLYQGFNS 180
 QY 181 VGGIITIRAAVFCGYDTAGKMLPDPKNTHTIVSWMTAQVTAAGVSPEDTVRRMM 240
 DB 181 VGGIITIRAAVFCGYDTAGKMLPDPKNTHTIVSWMTAQVTAAGVSPEDTVRRMM 240
 QY 241 QSGRKADIMYTGTVCMRKIFPDEGKAFKFGKAMSNVLRGMGAFVLYLDELKRYI 298
 DB 241 QSGRKADIMYTGTVCMRKIFPDEGKAFKFGKAMSNVLRGMGAFVLYLDELKRYI 298
 RESULT 4
 OSQSH5 PRELIMINARY; PRT; 298 AA.
 AC OSQSH5;
 DT 01-JUN-1998 (Tremblrel. 06, Created)
 DT 01-JUN-1998 (Tremblrel. 06, Last sequence update)
 DT 01-MAR-2003 (Tremblrel. 23, Last annotation update)
 DE ADP/ATP translocase.
 OS Oryctolagus cuniculus (Rabbit).
 OC Eukaryota; Metazoa; Chordata; Cranialata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Lagomorpha; Leporidae; Oryctolagus.
 NCBI_TaxID=9986;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC Tissue-Skeletal muscle;
 RA Yamaguchi N., Kasai M.;
 RT "Identification of a 30kDa calsequestrin-binding protein, which
 RT regulates calcium release from sarcoplasmic reticulum of rabbit
 RT skeletal muscle.";
 RL J. Biochem. 335:541-547(1998).
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
 DR EMBL; AB009386; BAA23777.1; -;
 DR Interpro: IPR001993; Mitoch_carrier.
 DR Interpro: IPR002067; Mit_carrier.
 DR Interpro: IPR002030; Mit_uncoupling.
 DR Pfam: PF00153; mito_carri; 3.
 DR PRINTS: PR00926; MITOCARRIER.
 DR PRINTS: PR00784; MTUNCOUPLING.

DB 1 MTDAAISFAKDFLAGGVAASIKTAVAPIERVKLLQVOHASKQITADKQKIMDCVVR 60
 QY 61 IPKEGVLSPFWRGNLANVIRYEPFQALNFAFKDKYQJFLGVDKHTQFWRYFAGNLASG 120
 DB 61 IPKEGVLSPFWRGNLANVIRYEPFQALNFAFKDKYQJFLGVDKHTQFWRYFAGNLASG 120
 QY 121 GAAGTSLCFEYVPLDFARTRLAADVGKSGTEREFGDGLCVLTKTSQDGINLQYGFVS 180
 DB 121 GAAGTSLCFEYVPLDFARTRLAADVGKSGTEREFGDGLCVLTKTSQDGINLQYGFVS 180
 QY 181 VOGIIYRAAYRGVYDFAKGMPLDPKNTIHVSWMIAGQVTVAVAGVSPPTVRRRMM 240
 DB 181 VOGIIYRAAYRGVYDFAKGMPLDPKNTIHVSWMIAGQVTVAVAGVSPPTVRRRMM 240
 QY 241 OSGRKADIMYTGVDCKWKIRIFRDEGKAFKFGANSNVLKMGAFVLVYDELKVI 298
 DB 241 OSGRKADIMYTGVDCKWKIRIFRDEGKAFKFGANSNVLKMGAFVLVYDELKVI 298

RESULT 10

Q95VX4 PRELIMINARY; PRT: 299 AA.
 AC 095VX4: 01-DEC-2001 (TREMBlrel. 19, Created)
 DT 01-DEC-2001 (TREMBlrel. 19, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE ADP-ATP translocator.
 OS Ethmostigmus rubripes.
 OC Eukaryota; Metazoa; Arthropoda; Myriapoda; Chilopoda;
 OC Pleurostigmophora; Scolopendromorpha; Scolopendridae; Ethmostigmus.
 RN NCBI_Taxid=62613;
 RP SEQUENCE FROM N.A.
 RA Burrell J.N.;
 RT "Nucleotide sequence of an ADP-ATP translocator of Ethmostigmus
 rubripes.";
 RL Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AF401758; AAL02100.1;
 DR InterPro; IPR001993; Mitoch_carrier.
 DR InterPro; IPR02067; Mit_carrier.
 DR Pfam; PF00153; mito_carr; 3.
 DR PRINTS; PR00926; MITOCH_CARRIER.
 DR PROSITE; PS00215; MITOCH_CARRIER; 3.
 DR PROSITE; PS00215; MITOCH_CARRIER; 3.
 SQ SEQUENCE 299 AA; 33037 MW; 3C3BCB26E7C3C5E CRC64;

Query Match 84.3%; Score 1300; DB 5; Length 299;
 Best Local Similarity 81.5%; Pred. No. 1.5e-109;
 Matches 243; Conservative 26; Mismatches 29; Indels 0; Gaps 0;

QY 1 MTEQAISFAKDFLAGGIAAISKTAIVAPIERVKLLQVOHASKQITADKQKIMDCVVR 60
 DB 1 MTEQAISFAKDFLAGGIAAISKTAIVAPIERVKLLQVOHASKQITADKQKIMDCVVR 60
 QY 61 IPKEGVLSPFWRGNLANVIRYEPFQALNFAFKDKYQJFLGVDKHTQFWRYFAGNLASG 120
 DB 61 IPKEGVLSPFWRGNLANVIRYEPFQALNFAFKDKYQJFLGVDKHTQFWRYFAGNLASG 120
 QY 121 GAAGTSLCFEYVPLDFARTRLAADVGKSGTEREFGDGLCVLTKTSQDGINLQYGFVS 180
 DB 121 GAAGTSLCFEYVPLDFARTRLAADVGKSGTEREFGDGLCVLTKTSQDGINLQYGFVS 180
 QY 181 VOGIIYRAAYRGVYDFAKGMPLDPKNTIHVSWMIAGQVTVAVAGVSPPTVRRRMM 240
 DB 181 VOGIIYRAAYRGVYDFAKGMPLDPKNTIHVSWMIAGQVTVAVAGVSPPTVRRRMM 240
 QY 241 OSGRKADIMYTGVDCKWKIRIFRDEGKAFKFGANSNVLKMGAFVLVYDELKVI 298
 DB 241 OSGRKADIMYTGVDCKWKIRIFRDEGKAFKFGANSNVLKMGAFVLVYDELKVI 298

RESULT 11
 Q91336 PRELIMINARY; PRT: 317 AA.

AC Q91336; 01-NOV-1996 (TREMBlrel. 01, Created)
 DT 01-NOV-1996 (TREMBlrel. 01, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE ADP-ATP translocase.
 OS Rana sylvatica (Wood frog).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Amphibia; Batrachia; Anura; Neobatrachia; Ranioidea; Rana.
 RN NCBI_Taxid=45438;
 RP SEQUENCE FROM N.A.
 RA Cai O.; Greenway S.C.; Storey K.B.;
 RT "Differential regulation of the mitochondrial ADP/ATP translocase gene
 in wood frogs under freezing stress".
 RL Biochim. Biophys. Acta 1353:69-78(1997).
 RN [1]
 RP SEQUENCE FROM N.A.
 RA Cai O.; Storey K.B.;
 RT Submitted (APR-1999) to the EMBL/GenBank/DBJ databases.
 CC -1. SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
 DR EMBL; U44832; AAA97882.2;
 DR InterPro; IPR001993; Mitoch_carrier.
 DR InterPro; IPR02067; Mit_carrier.
 DR Pfam; PF00153; mito_carr; 3.
 DR PRINTS; PR00926; MITOCH_CARRIER.
 DR PROSITE; PS00215; MITOCH_CARRIER; 3.
 DR PROSITE; PS00215; MITOCH_CARRIER; 3.
 DR Membrane; Transmembrane; Transport.
 SQ SEQUENCE 317 AA; 35005 MW; 5F66B7BD8D5CEB72 CRC64;

Query Match 81.6%; Score 1259; DB 13; Length 317;
 Best Local Similarity 86.8%; Pred. No. 8.2e-106;
 Matches 236; Conservative 19; Mismatches 17; Indels 0; Gaps 0;

QY 1 MTEQAISFAKDFLAGGIAAISKTAIVAPIERVKLLQVOHASKQITADKQKIMDCVVR 60
 DB 1 MTEQAISFAKDFLAGGIAAISKTAIVAPIERVKLLQVOHASKQITADKQKIMDCVVR 60
 QY 61 IPKEGVLSPFWRGNLANVIRYEPFQALNFAFKDKYQJFLGVDKHTQFWRYFAGNLASG 120
 DB 61 IPKEGVLSPFWRGNLANVIRYEPFQALNFAFKDKYQJFLGVDKHTQFWRYFAGNLASG 120
 QY 121 GAAGTSLCFEYVPLDFARTRLAADVGKSGTEREFGDGLCVLTKTSQDGINLQYGFVS 180
 DB 121 GAAGTSLCFEYVPLDFARTRLAADVGKSGTEREFGDGLCVLTKTSQDGINLQYGFVS 180
 QY 181 VOGIIYRAAYRGVYDFAKGMPLDPKNTIHVSWMIAGQVTVAVAGVSPPTVRRRMM 240
 DB 181 VOGIIYRAAYRGVYDFAKGMPLDPKNTIHVSWMIAGQVTVAVAGVSPPTVRRRMM 240
 QY 241 OSGRKADIMYTGVDCKWKIRIFRDEGKAFKFGANSNVLKMGAFVLVYDELKVI 298
 DB 241 OSGRKADIMYTGVDCKWKIRIFRDEGKAFKFGANSNVLKMGAFVLVYDELKVI 298

RESULT 12
 Q81RA0 PRELIMINARY; PRT: 312 AA.
 AC 081RA0; 01-MAR-2003 (TREMBlrel. 23, Created)
 DT 01-MAR-2003 (TREMBlrel. 23, Last sequence update)
 DT 01-MAR-2003 (TREMBlrel. 23, Last annotation update)
 DE CG16944-PC.
 GN SEB.
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydroidea; Drosophilidae; Drosophila.
 RN NCBI_Taxid=7227;
 RP SEQUENCE FROM N.A.

RX MEDLINE-20196006; PubMed-10731132;
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Ananthites P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.F.,
 RA George R.A., Lewis S.J., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Mortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brannon R.C., Rogers J.H., Blazer R.G., Champe C., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Helt G., Nelson C.R., Gaber G.L.,
 RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,
 RA Ballew R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman J.P., Bhandari D., Bolshakov S.,
 RA Borokov D., Botchan M.R., Bouck J., Brokstein P., Brotler P.,
 RA Burris K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
 RA de Pablos B., Delcher A., Deng Z., Mays A.D., Dew I., Dietz S.M.,
 RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Fostel C., Gabrielian A.E., Garg N.S., Gelbart W.M., Glasser K.,
 RA Glodok A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,
 RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C.,
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Ketchum K.A.,
 RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
 RA Lasko P., Lei Y., Levitsky A.A., Li J., Li Z., Liang Y., Lin X.,
 RA Liu X., Mattei B., McIntosh T.C., McLeod M.P., McPherson D.,
 RA Merkulov G., Mishina N.V., Mobarry C., Morris J., Moshneft A.,
 RA Mount S.M., Moy M., Murphy B., Murphy L., Muzny D.M., Nelson D.L.,
 RA Nelson D.R., Nelson K.A., Nixon K., Nusskern D.R., Pacle J.M.,
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,
 RA Rainett K., Remington K., Saunders R.D., Scheeler F., Shen H.,
 RA Shue B.C., Siden-Kiamos I., Simpson M., Skupski M.P., Smith T.,
 RA Spletter E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svirskas R., Tector A.C., Turner R., Venter E., Wang A.H., Wang X.,
 RA Wang Z.Y., Wassarman D.A., Weinstock G.M., Weissbach J.,
 RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,
 RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao O., Zheng L.,
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.;
 RT "The genome sequence of *Drosophila melanogaster*.";
 RL Science 287:2185-2195(2000).
 [12]
 RN SEQUENCE FROM N.A.
 RA Celniker S.E., Adams M.D., Krommler B., Wan K.H., Holt R.A.,
 RA Evans C.A., Gocayne J.D., Ananthites P.G., Brannon R.C., Rogers Y.,
 RA Banzon J., An H., Baldwin D., Banzon J., Beeson K.Y., Busam D.A.,
 RA Carlson J.W., Center A., Champe M., Davenport L.B., Dietz S.M.,
 RA Dodson K., Dorsett V., Doup L.E., Doyle C., Dresnek D., Farfan D.,
 RA Ferreira S., Frise E., Galle R.F., Garg N.S., George R.A.,
 RA Gonzalez M., Houck J., Hoskins R.A., Hostin D., Howland T.J.,
 RA Idegami C., Jalali M., Kruse D., Li P., Mattei B., Moshneft A.,
 RA McIntosh T.C., Moy M., Murphy B., Nelson C., Nelson K.A., Nunoo J.,
 RA Pacle J., Paragas V., Park S., Patel S., Pfeiffer B.,
 RA Phouenavong S., Pittman G.S., Puri V., Richards S., Scheeler F.,
 RA Stapleton M., Strong R., Svirskas R., Tector C., Tyler D.,
 RA Williams S.M., Zaveri J.S., Smith H.O., Venter J.C., Rubin G.M.;
 RT "Sequencing of *Drosophila melanogaster* genome.";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 [13]
 RN SEQUENCE FROM N.A.
 RA Misra S., Crosby M.A., Matthews B.B., Bayraktaroglu L., Campbell K.,
 RA Hradecky P., Huang Y., Kaminker J.S., Prochuk S.E., Smith C.D.,
 RA Tupy J.L., Bergman C., Berman B., Carlson J.W., Celniker S.E.,
 RA Ciamp M., Dysdale R., Emmert D., Frise E., de Grey A., Harris N.,
 RA Krommler B., Marshall B., Millburn G., Richter J., Russo S.,
 RA Searle S.M.J., Smith E., Shu S., Smutnak F., Whitfield E.,
 RA Ashburner M., Gelbart W.M., Rubin G.M., Mungall C.J., Lewis S.E.;
 RT "Annotation of *Drosophila melanogaster* genome.";
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 [14]
 RN SEQUENCE FROM N.A.
 RA Adams M.D., Celniker S.E., Gibbs R.A., Rubin G.M., Venter C.J.;
 RL Submitted (MAR-2000) to the EMBL/GenBank/DBJ databases.
 [15]
 RN SEQUENCE FROM N.A.

RA flyBase;
 RL Submitted (SEP-2002) to the EMBL/GenBank/DBJ databases.
 DR EMBL: AEO03484; AAN09267.1; -
 SO SEQUENCE 312 AA; 34214 MW; 78D5634E74E1680F CRC64;
 Query Match 81.3%; Score 1254.5; DB 5; Length 312;
 Best Local Similarity 80.6%; Pred. No. 2.1e-105;
 Matches 237; Conservative 23; Mismatches 33; Indels 1; Gaps 1;
 5 AISPADFLAGGIAAIAISKTAIVAPIERVKLLLOVHASKIOADKQKIVDQIVRPRKE 64
 20 AAGVADPEAAGGISAASKTAIVAPIERVKLLLOVHASKIOISPKQYKGVADCFIRPKKE 79
 65 OGVLSEFMRGNLANVIRYPTQALNFAFKDKYKQIFLGGVDRHTQFMRFFGNLASGAAG 124
 80 OGFSFMRGNLANVIRYPTQALNFAFKDKYKQIFLGGVDRHTQFMRFFGNLASGAAG 139
 125 ATSLCFYPLDFAFTRIAADVGKSGTERERGLDCLVKTIKSDGIRGLYOGFSVVOGI 184
 140 ATSLCFYPLDFAFTRIAADVGKSG-OREFTGLGNCITLKIFKSDGIRGLYOGFSVVOGI 198
 185 IIRAAVFGYDPAKGLPDKNTHYVSMIAQOTVAVAGVSYPTDVRBRMMQSGR 244
 IIRAAVFGYDPAKGLPDKNTHYVSMIAQOTVAVAGVSYPTDVRBRMMQSGR 258
 245 KGADIMYTGTVDCRKIFRDEGGKAFKGAWSNVLRCMGAFVLYVDELKRYI 298
 259 KAEVYIKNTLHCWATIAKQEGAFKGFNSILRGTGAFVLYVDELKRYI 312
 RESULT 13
 ID 09NHMS PRELIMINARY; PRT; 300 AA.
 AC 09NHMS
 DT 01-OCT-2000 (TrEMBLrel. 15, Created)
 DT 01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
 DT 01-MAR-2003 (TrEMBLrel. 23, Last annotation update)
 DE ADP/ATP translocase.
 OS Lucilia cuprina (Greenbottle fly) (Australian sheep blowfly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Oestroidea;
 OC Calliphoridae; Lucilia.
 OX NCBI_TaxID=7375;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC STRAIN=SS mal seeking;
 RT "A cDNA clone encoding the ADP/ATP translocase of *Lucilia cuprina*.";
 RL Submitted (DEC-1999) to the EMBL/GenBank/DBJ databases.
 CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
 DR EMBL: AF218587; AAF32322.1; -
 DR InterPro: IPR001993; Mitochondrion carrier.
 DR InterPro: IPR002067; Mitochondrion carrier.
 DR Pfam: PF00153; Mitochondrion carrier.
 DR PRINTS: PR00926; MITOCHARRIER.
 DR PROSITE: PS00215; MITOCHARRIER.
 KM Membrane; Transmembrane; Transport.
 SO SEQUENCE 300 AA; 33036 MW; 5459DF0EA0E2E742 CRC64;
 Query Match 80.1%; Score 1235.5; DB 5; Length 300;
 Best Local Similarity 79.5%; Pred. No. 1e-103;
 Matches 233; Conservative 24; Mismatches 35; Indels 1; Gaps 1;
 6 ISPAKDFLAGGIAAIAISKTAIVAPIERVKLLLOVHASKIOADKQKIVDQIVRPRKE 65
 9 LGFVKDFPAAGGISAASKTAIVAPIERVKLLLOVHASKIOISPKQYKGVADCFIRPKKE 68
 66 GVLSEFMRGNLANVIRYPTQALNFAFKDKYKQIFLGGVDRHTQFMRFFGNLASGAAGA 125
 69 GFSFMRGNLANVIRYPTQALNFAFKDKYKQIFLGGVDRHTQFMRFFGNLASGAAGA 128
 126 TSLCFYPLDFAFTRIAADVGKSGTERERGLDCLVKTIKSDGIRGLYOGFSVVOGI 185

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DB 129 TSLCFVYPLDPFARRRLAADTKG-QREFTLGNCIAKIFKSDGLVGLRGHVSVCII 187
QY 186 IYRAAYGVYDTAKGMLPDPKNTIIVSWMIQOTVAVAGVSPEDTFRRRMMQSGRK 245
DB 188 IYRAAYGVYDTAKGMLPDPKNTIIVSWMIQOTVAVAGVSPEDTFRRRMMQSGRK 247
QY 246 GADIMYGTGVDCWKIRIFDEGKAFKFGAGSNVLRGMGAFVLYLDELKVI 298
DB 248 ATEIITKNTLHCWMTIAKOE-GSAFFKAGFASNVLRGTGAFVLYLDEIKKFL 300

RESULT 14
ID 044093 PRELIMINARY; PRT; 288 AA.
AC 044094;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)
DE ADP/ATP translocase (Fragment).
GN SE8B.
OS Drosophila pseudoobscura (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7237;
RN [1]
RP SEQUENCE FROM N.A.
RA Zeng L.-W., Comeron J.M., Chen B., Kreitman M.;
RL Genetics 0:0-0(1997).
CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
DR EMBL; AF025799; AAB87884.1; -.
DR Flybase; FBgn0023292; Dpse\se8b.
DR InterPro; IPR001993; Mitoch_carrier.
DR InterPro; IPR002067; Mit_carrier.
DR Pfam; PF00153; mito_carr; 3.
DR PRINTS; PR00926; MITOCARRIER.
DR PROSITE; PS00215; MITOCH_CARRIER; 3.
DR Membrane; Repeat; Transmembrane; Transport.
KW NON_TER 288
FT SEQUENCE 288 AA; 31725 MW; 052B0CC0050436B0 CRC64;
SQ

Query Match 77.0%; Score 1187.5; DB 5; Length 288;
Best Local Similarity 80.7%; Pred. No. 2.2e-99;
Matches 230; Conservative 19; Mismatches 33; Indels 3; Gaps 3;

QY 5 AISEFAKDLAGGIAAISKTAAPIERVKLLQVOHASKQIADQYGIYDCIYRIKE 64
DB 7 AMGFVKDPAAGGISAASVKTAAPIERVKLLQVOHISKQISPDKQYGMVDCFTIRIKE 66
QY 65 QGVLSFWRGNLNANVIRYPTQALNFAFDKYYKOIFLGGVDKHTQFWRYFAGNLAGGAAG 124
DB 67 QGFSSEFWGNLANVIRYPTQALNFAFDKYYKOIFLGGVDKHTQFWRYFAGNLAGGAAG 126
QY 125 ATSLCFVYPLDPFARRRLAADVGKSGTEREPRGLDCLVYKTSKDSIRGLYOGFSVVOGI 184
DB 127 ATSLCFVYPLDPFARRRLAADVGKSGTEREPRGLDCLVYKTSKDSIRGLYOGFSVVOGI 185
QY 185 IYRAAYGVYDTAKGMLPDPKNTIIVSWMIQOTVAVAGVSPEDTFRRRMMQSGR 244
DB 186 IYRAAYGVYDTAKGMLPDPKNTIIVSWMIQOTVAVAGVSPEDTFRRRMMQSGR 244
QY 245 KGADIMYGTGVDCWKIRIFDEGKAFKFGAGSNVLRGMGAFVLY 289
DB 245 KATEIITKNTLHCWMTIAKOE-GSAFFKAGFASNVLRGTGAFVLY 288

RESULT 15
ID 044094 PRELIMINARY; PRT; 288 AA.
AC 044094;
DT 01-JUN-1998 (TREMBLrel. 06, Created)
DT 01-JUN-1998 (TREMBLrel. 06, Last sequence update)
DT 01-MAR-2003 (TREMBLrel. 23, Last annotation update)

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DE ADP/ATP translocase (Fragment).
GN SE8B.
OS Drosophila subobscura (Fruit fly).
OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
OC Ephydroidea; Drosophilidae; Drosophila.
OX NCBI_TaxID=7241;
RN [1]
RP SEQUENCE FROM N.A.
RA Zeng L.-W., Comeron J.M., Chen B., Kreitman M.;
RL Genetics 0:0-0(1997).
CC -1- SIMILARITY: BELONGS TO THE MITOCHONDRIAL CARRIER FAMILY.
DR EMBL; AF025799; AAB87884.1; -.
DR Flybase; FBgn0023237; Dsub\se8b.
DR InterPro; IPR001993; Mitoch_carrier.
DR InterPro; IPR002067; Mit_carrier.
DR Pfam; PF00153; mito_carr; 3.
DR PRINTS; PR00926; MITOCARRIER.
DR PROSITE; PS00215; MITOCH_CARRIER; 3.
DR Membrane; Repeat; Transmembrane; Transport.
KW NON_TER 288
FT SEQUENCE 288 AA; 31775 MW; 06A1D1E477E81B26 CRC64;
SQ

Query Match 76.7%; Score 1183.5; DB 5; Length 288;
Best Local Similarity 80.4%; Pred. No. 5e-99;
Matches 229; Conservative 20; Mismatches 33; Indels 3; Gaps 3;

QY 5 AISEFAKDLAGGIAAISKTAAPIERVKLLQVOHASKQIADQYGIYDCIYRIKE 64
DB 7 AMGFVKDPAAGGISAASVKTAAPIERVKLLQVOHISKQISPDKQYGMVDCFTIRIKE 66
QY 65 QGVLSFWRGNLNANVIRYPTQALNFAFDKYYKOIFLGGVDKHTQFWRYFAGNLAGGAAG 124
DB 67 QGFSSEFWGNLANVIRYPTQALNFAFDKYYKOIFLGGVDKHTQFWRYFAGNLAGGAAG 126
QY 125 ATSLCFVYPLDPFARRRLAADVGKSGTEREPRGLDCLVYKTSKDSIRGLYOGFSVVOGI 184
DB 127 ATSLCFVYPLDPFARRRLAADVGKSGTEREPRGLDCLVYKTSKDSIRGLYOGFSVVOGI 185
QY 185 IYRAAYGVYDTAKGMLPDPKNTIIVSWMIQOTVAVAGVSPEDTFRRRMMQSGR 244
DB 186 IYRAAYGVYDTAKGMLPDPKNTIIVSWMIQOTVAVAGVSPEDTFRRRMMQSGR 244
QY 245 KGADIMYGTGVDCWKIRIFDEGKAFKFGAGSNVLRGMGAFVLY 289
DB 245 KATEIITKNTLHCWMTIAKOE-GTAFKAGFASNVLRGTGAFVLY 288

Search completed: August 28, 2003, 19:42:11
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